BIT Life Sciences' 3rd World Congress of Vaccine
Beijing·China

Session Name: Section 2-2-1: Bioinformatics, Antigen Design, and Vaccine Development

Decoding non-coding Dna Codes: Human Genome Meta-Chromosomes Architecture

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support Pr ***Luc Montagnier*** *FMPRS World AIDS Foundation UNESCO*
and ***Jean-rené Fourtou*** *Vivendi Universal chairman*

More on: http://golden-ratio-in-dna.blogspot.com/

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- **Part I - BACKGROUND:**
- DNA supracode (1991-1997)
- Human genome Codon populations: Numbers and atomic weighs perfect balancing (2004-2009)
- **Part II - RESULTS:**
- Whole Human Genome Codon Populations reveals central rôle of « Phi » the « Golden ratio » J.C. Perez - Interdiscip Sci Comput Life Sci (2010) 2: 1–13 DOI: 10.1007/s12539-010-0022-0« Codon Populations in Single-stranded Whole Human Genome DNA Are Fractal and Fine-tuned by the Golden Ratio 1.618 » (2010)
- Proof of a Functional Human Chromosomes Meta-structure involving « Pi » and « Phi » Universal Constants (2010).
- **Part III - FUTURES:**
- The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes: Binary Code and Waveforms in DNA... *« Is there an Equation for Life »?* (1997-2003)
- Perspectives in Luc Montagnier's *« DNA Waves and Water »* breakthrough Luc Montagnier ,Lindau NOBELS conference, 28 June, 2010 - DNA BETWEEN PHYSICS AND BIOLOGY: « DNA WAVES AND WATER » (2011).

$$\text{Proj}\,(m) = [\ 1 - [\ 4\pi\sqrt{\varphi}\varphi\varphi^2\ ]\ ]\ m$$

with: $\sqrt{\varphi}=1/\sqrt{\Phi}$ *Phi is the GOLDEN RATIO* Φ

$\varphi = 1/\Phi$

$\varphi^2 = 1/\Phi^2$

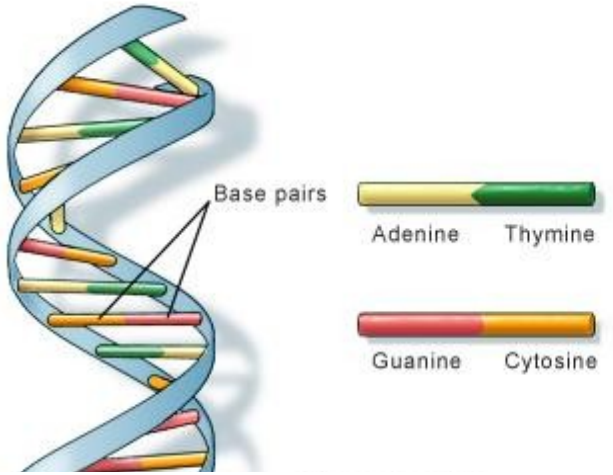
« Why are there Numbers in the Nature? »

Alan Turing...

The Chemical Basis of Morphogenesis A. M. Turing

Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences, Vol.237, No. 641. (Aug. 14, 1952), pp. 37-72.

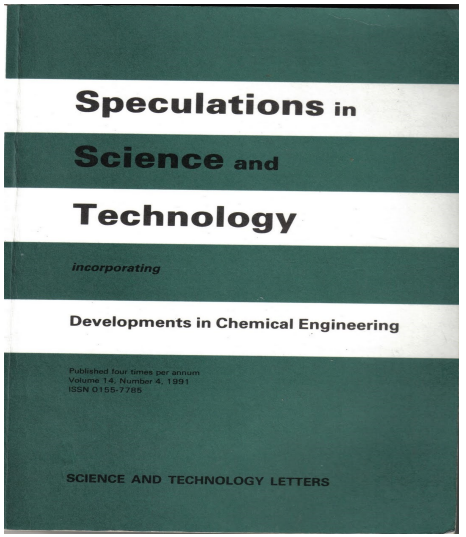
1 2 3 4... Pi... Phi...

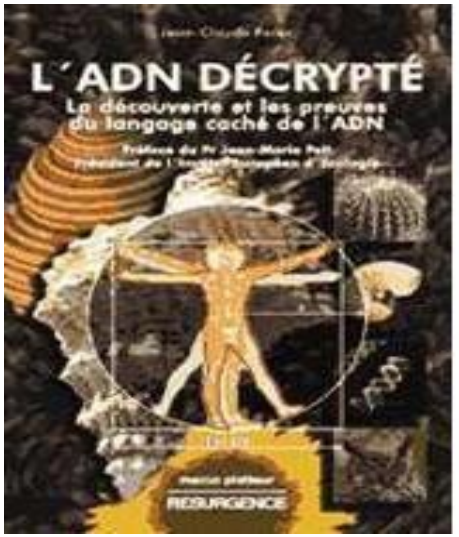


Numbers...
Codes...
Atomic
Weights...
Waves...

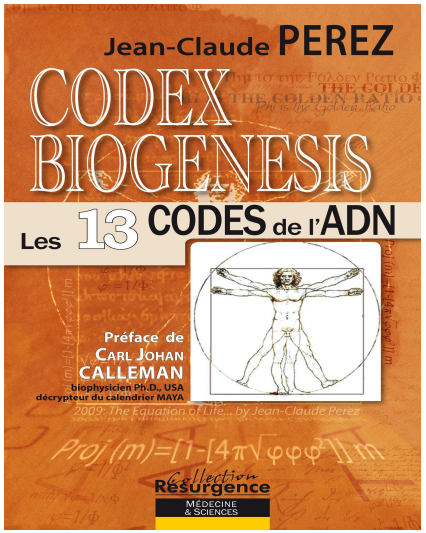
90% of this conference contents provide from 2 publications (1991 and 2010) and from 2 french books (1997 and 2009)...

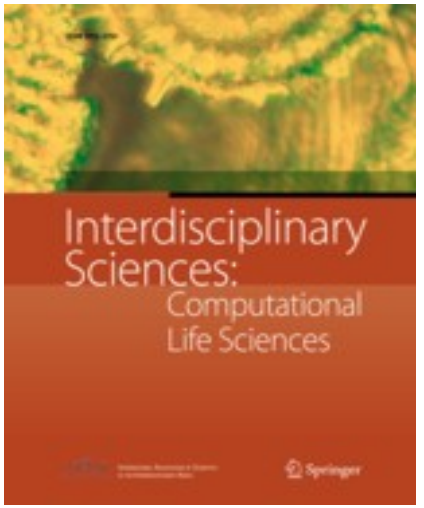
1991 and 1997...





2009 and 2010...





2010: Eric Lander (Science Adviser to the President and Director of Broad Institute) et al. Published a ***FRACTAL structure of DNA at a PHYSICAL LEVEL*** and delivered this message on Science Magazine coversheet (Oct. 9, 2009) to the effect:

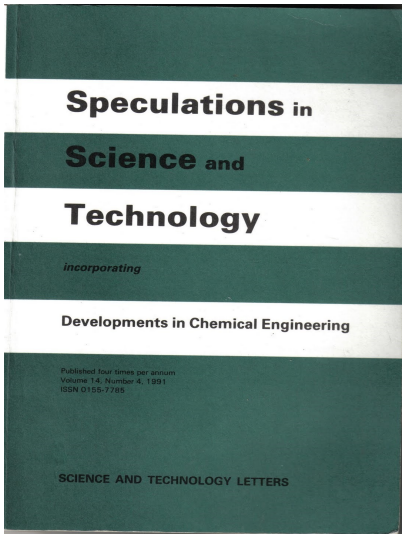
"Mr. President; The Genome is Fractal ! »

In 1991 – about 20 years ago – we published « DNA supracode »

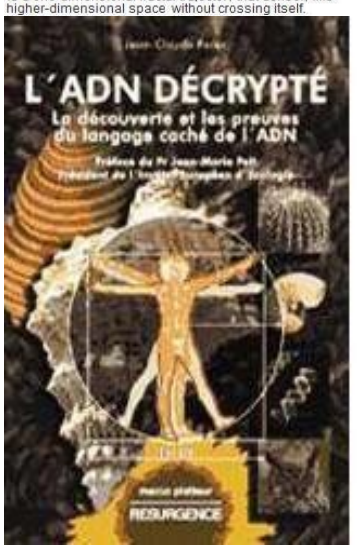
In 1991 (1) then in 1997 (2), ***we proposed a FRACTAL structure od genes-coding DNA at a LOGICAL LEVEL...***

Ref 1: J.C. Perez - "Chaos DNA and Neuro-computers : a golden link / The hidden language of genes, global language and ordre in the human genome", in Speculations in Science and Technology, vol 14 number 4 1991, ISSN 0155-7785.

Ref 2: Jean-claude Perez, L'ADN DECRYPTE (DNA DECODED), (1997) Marco Pietteur publishing (Resurgence collection) Embourg Belgium, ISBN 2-87211-017-8 (in french)



First described by David Hilbert in 1891, the Hilbert curve is a one-dimensional fractal trajectory that densely fills higher-dimensional space without crossing itself.

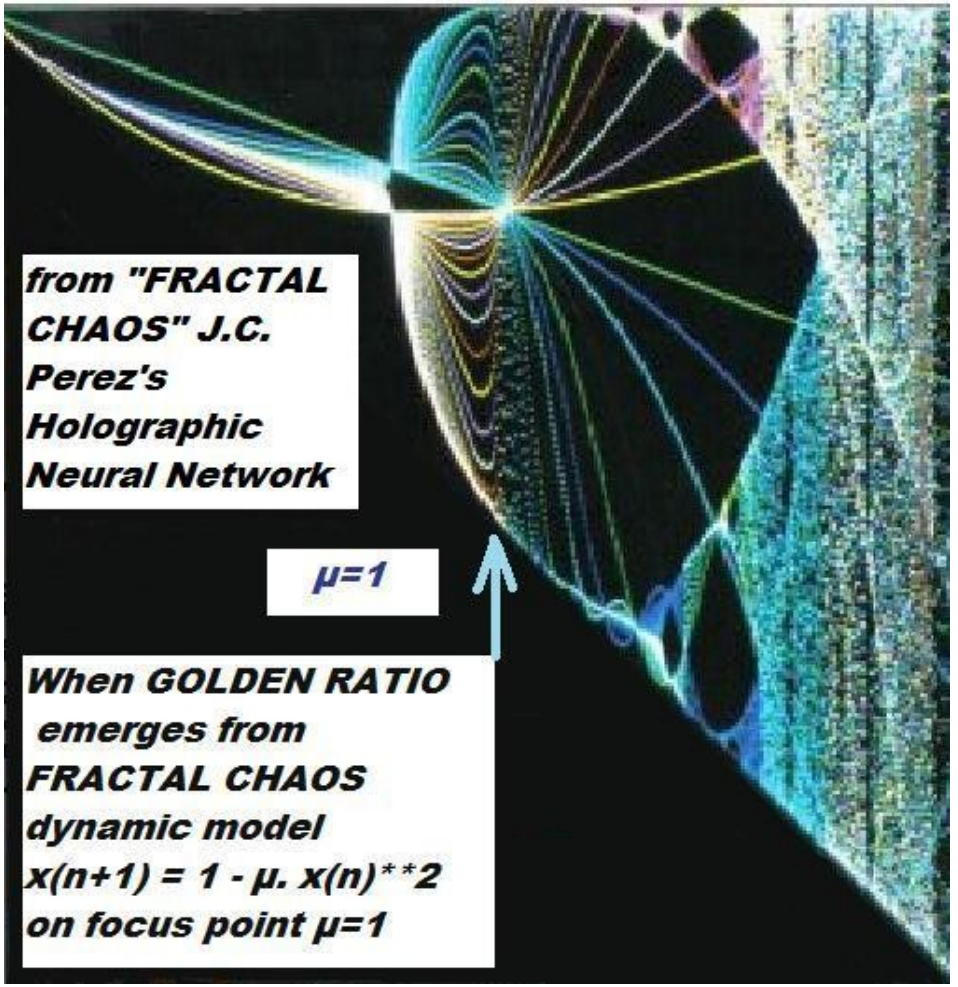


DNA supracode genesis:

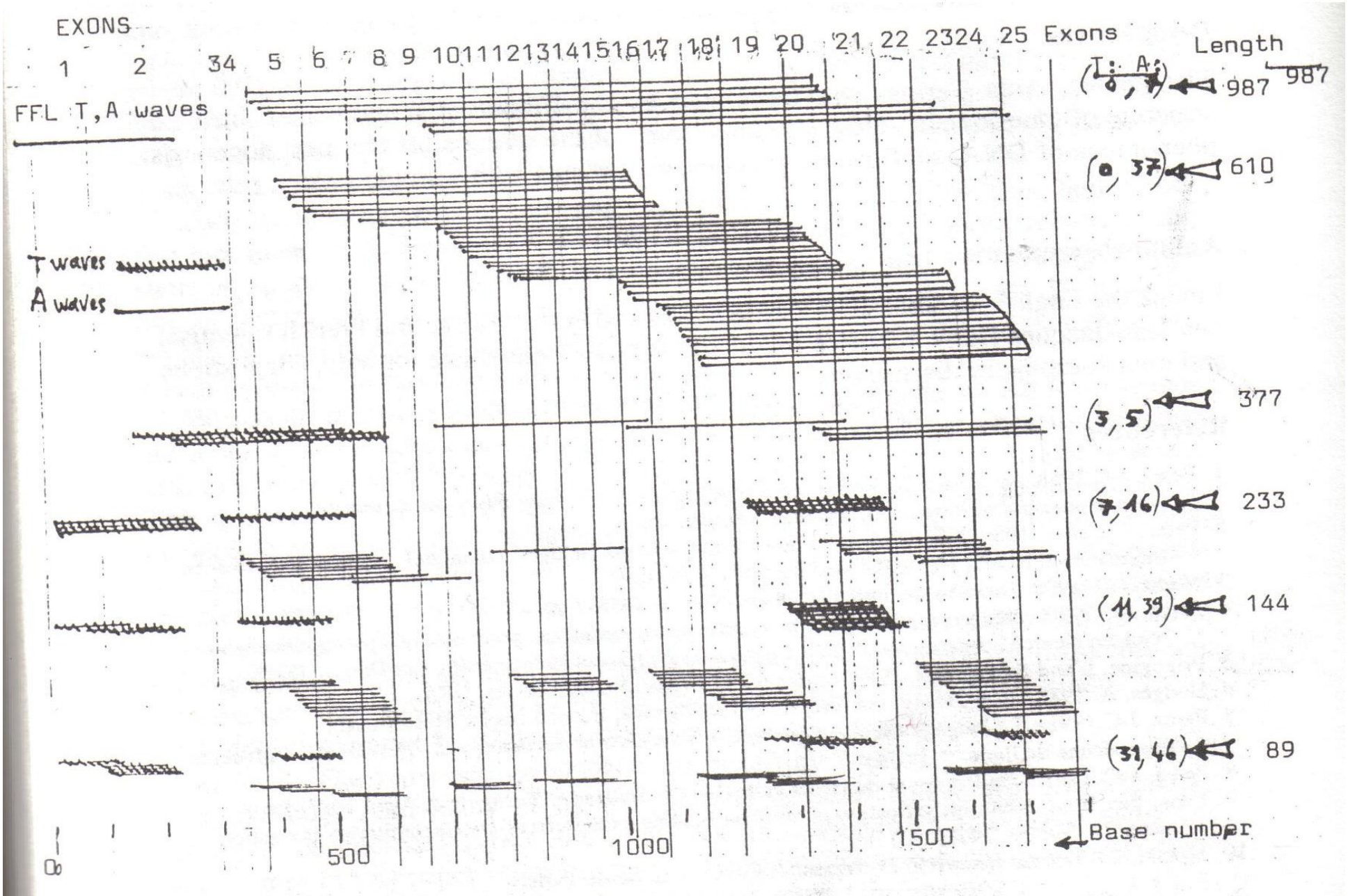
- 1 - Working on neuro-computers we discovered an hypersensitivity of FRACTALS aroung the GOLDEN RATIO area (with Golden ratio Phi=1.618033... as 1/Phi = 1+Phi).
-2- FIBONACCI numbers ratios are GOLDEN RATIO like proportions!
-3- Then we think: *« what about FIBONACCI numbers nucleotides proportions in DNA sequences? »*
-4- a **« resonance »** is by example: 55 T and 89 CAG in 144 bases TACG.

- In 1991 we proposed that Golden Ratio and Fibonacci/Lucas integer numbers define strong relationships between DNA gene-coding region sequences and Fibonacci's embedded TCAG gene sequence patterns. We also prove the optimality of these patterns in the book L'ADN décrypté ("Deciphering DNA").

- Examples involving evolution and pathogen analysis include genes or small gene-rich genomes, especially the HIV genome. This book explores a numerical property called the "DNA Supracode" consisting of exhaustive combinatorial research of "resonances" within gene-coding DNA sequences: a resonance is a harmonious proportion of exact Fibonacci/Lucas nucleotide numbers. For example: 144 contiguous TCAG nucleotides have exactly 55 T nucleotides and 89 A or C or G nucleotides. Then a resonance exists with an the Golden ratio: 55, 89 and 144 are consecutive Fibonacci numbers following the Golden Ratio. Gene-rich genomes like HIV have thousands of "resonances", where the longer ones overlap 2/3rds of the whole genome length.



DNA supracode and Fibonacci serie: 1 1 2 3 5 8 13 21 34 55 89...
Example of resonances in HUMC1A1 gene



The Number « 2 » in Nature

Alan Turing: why are there Numbers in the Nature?
Example of the MENDELEIEV PERIODIC TABLE

In 2009, We proposed in the book CODEX BIOGENESIS a very simple numerical formula computing the number of elements within every period then, finally, within the whole structure:

c(p) = 2 [Int ((p+2) / 2)]2**

(where p is the period number, c(p) is the number of Elements within the period layer and Int(x) is the integer whole value of real number x). Examples :

If p=1 ➔ c(1)=2

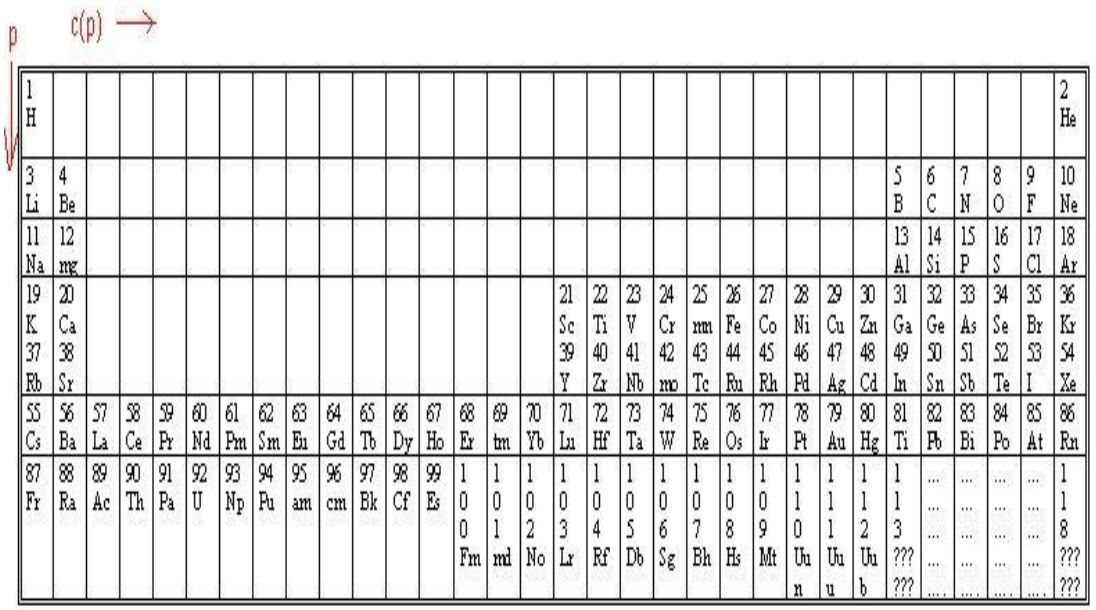
If p=2 ➔ c(2)=8 If p=3 ➔ c(3)=8

If p=4 ➔ c(4)=18 If p=5 ➔ c(5)=18

If p=6 ➔ c(6)=32 If p=7 ➔ c(7)=32

If p=8 ➔ c(8)=50 If p=9 ➔ c(9)=50

…/… If p=16 ➔ *c(16)=162*



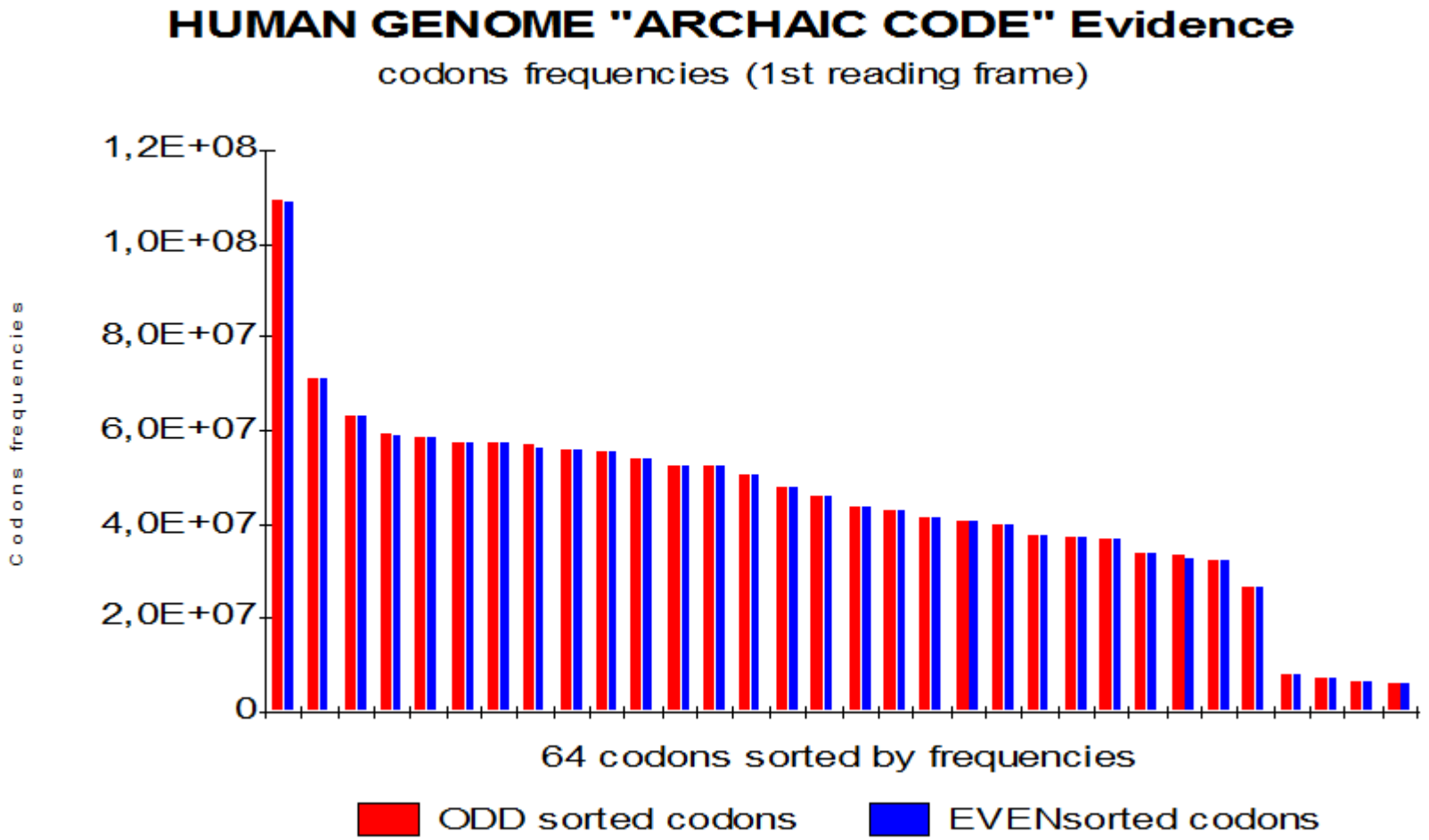
$$c(p) = 2 \cdot [Int(\frac{p+2}{2})]^2$$

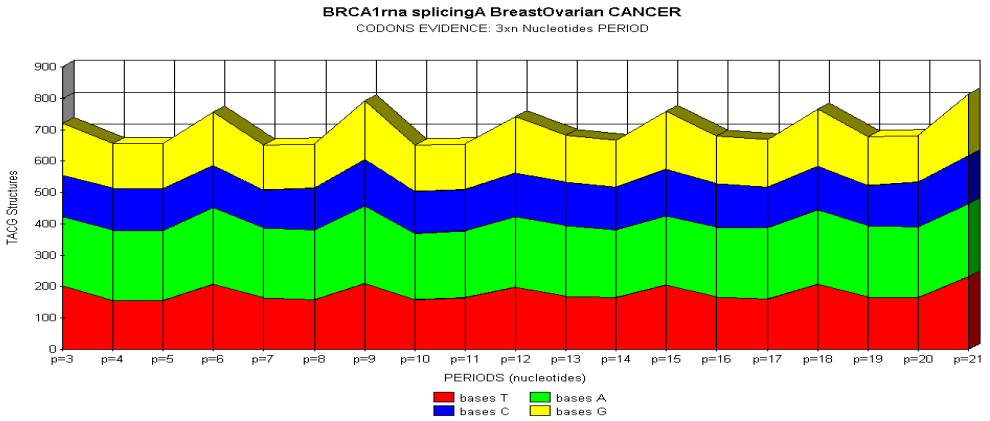
The Predictive Formula of Mendeleiev's PERIODIC TABLE by J.C. Perez

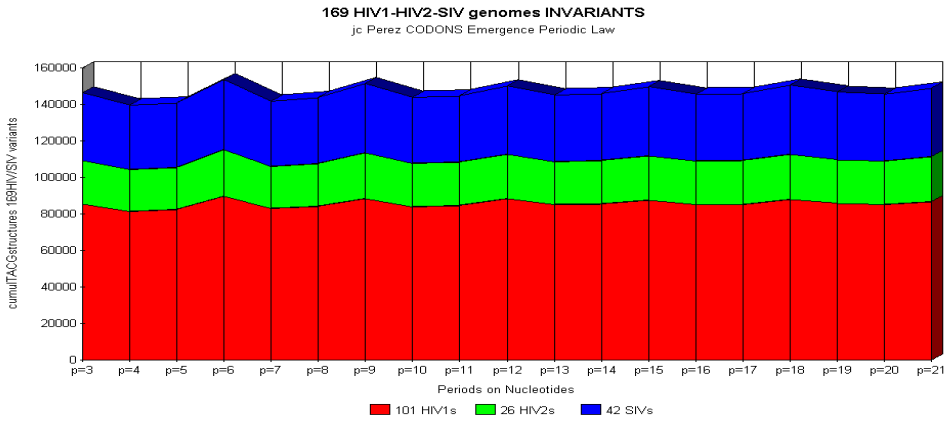
Ref: Jean-claude Perez, CODEX BIOGENESIS (2009) Marco Pietteur publishing (Resurgence collection) Embourg Belgium, ISBN 2874340448 pages 47-70 (in french)

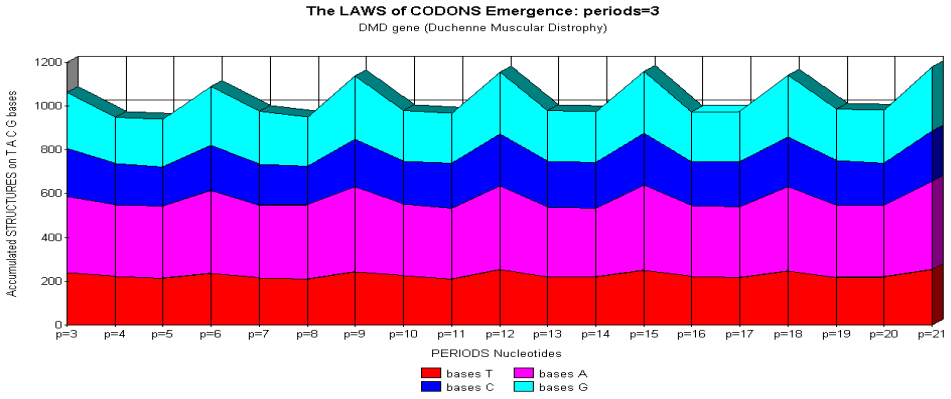
The Number « 2 » in DNA

Alan Turing: why are there Numbers in the Nature?
Example of the discovery of « TWIN MIRROR-CODONS »
in simple stranded whole Human Genome DNA









The Number « 3 »

- ***« Why a Triplet ?***

We have argued that the code must have been basically a triplet code from a very early stage, so that one is not entitled to use sophisticated arguments which would apply only to a later stage, although one could argue that early organisms with doublet or quadruplet codes actually existed but became extinct, only the triplet code surviving. … / … It must have, to some extent, a definite structure and this is likely to be based on stretches of double-helix. Thus,the diameter of a double.helix (since two may have to lie side by side) may have dictated the size of the codon, in that a doublet-code (moving along two bases at a time) would present an impossible recognition problem. »

F. H. C. CRICK in « The Origin of the Genetic Code », published in 1968, *J. Mol. Biol.* (1968) 38, 367-379.

OUR RESPONSE: Doing DNA sequence reshapings: modulo2 (2 columns array), modulo3 (3 columns array), modulo »n » (« n » columns array)... We discovered typical tops for modulo3 multiples numbers (3 6 9 12 15...).

THEN:

there is an evidence of DNA sequences shaded organization in triplets (coding and uncoding DNA)!

The Number « 4 »: Doing a 4-partition of single-stranded whole Human Genome DNA Codon populations

ODD range sorted codons		EVEN range Sorted codons	
QUARTILE 1 : 316027664		QUARTILE 2 : 315402427	
36530115	TTT	AAA	36381293
23669701	ATT	AAT	23634011
20990387	TCT	AGA	20948987
19750578	TTA	TAA	19721149
19568343	TAT	ATA	19548709
19195946	CTG	CAG	19176935
19152113	TGT	ACA	19073189
18944797	CTT	AAG	18894716
18708048	TTC	GAA	18678084
18565027	TCA	TGA	18562015
18005020	TTG	CAA	17927956
17480496	TGG	CCA	17444649
17423117	CAT	ATG	17409063
16835177	CCT	AGG	16810797
15942742	CTC	GAG	15939419
15266057	AGT	ACT	15251455
QUARTILE 3: 158309529		QUARTILE 4 : 1580642247	
14619310	GGA	TCC	14614789
14252868	GTG	CAC	14214421
13852086	GTT	AAC	13794251
13649076	TGC	GCA	13635427
13252828	GCT	AGC	13242724
12658530	GAT	ATC	12650299
12446600	GGG	CCC	12428986
12240281	TAG	CTA	12217331
11268094	GCC	GGC	11258126
11026602	GGT	ACC	11007307
10766854	GTA	TAC	10755607
8955434	GTC	GAC	8938833
2606672	CCG	CGG	2604253
2379612	CGT	ACG	2372235
2247440	GCG	CGC	2244432
2087242	TCG	CGA	2085226
Cumulated ODD codons		Cumulated EVEN codons	
474337193		473466674	

Number « 4 »...1 2 3 5 6...

The 4 « quartiles »:

Q1= 316027664 bases Q2= 315402427 bases

Q3= 158309529 bases Q4= 158064247 bases

if we consider 2 clusters of 32 codon populations each, the most frequent (Q1+Q2) is exactly 2X as numerous as the least frequent of the 32 codons (Q3+Q4) . Exact ratio is 1.995859355

Ratios Integer Numbers

The Number « 1 » (Q1+Q3)÷(Q2+Q4) =1.001838607

The Number « 2 » (Q1+Q2)÷(Q3+Q4) =1.995835745

The Number « 3 » (Q1+Q2+Q3+Q4)÷Q1 =2.99911677

(Q1+Q2+Q3+Q4)÷Q2=3.00506206

(Q1+Q2+Q3+Q4)÷(Q3+Q4)=2.995835745

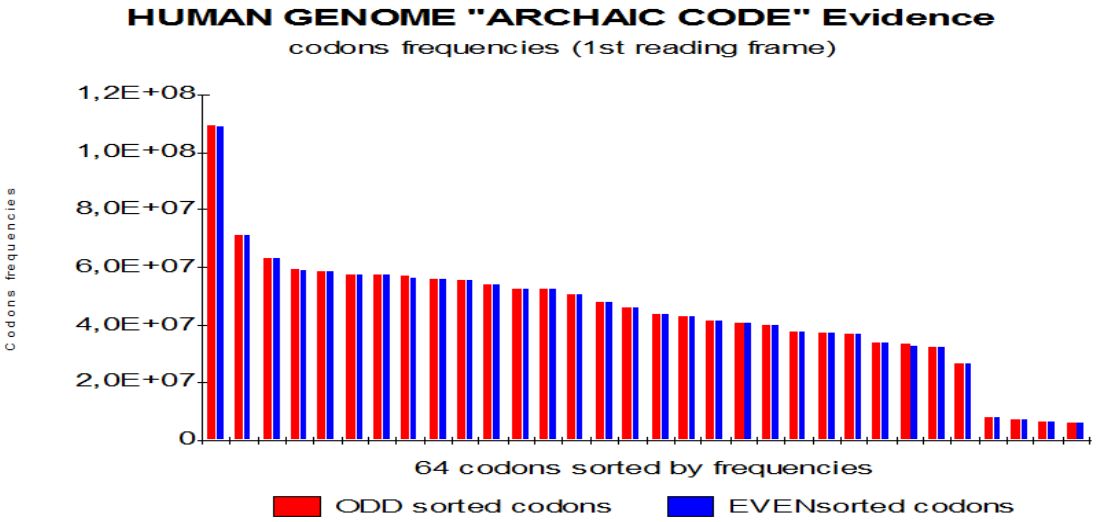
The Number « 4 » (Q1+Q2)÷(Q4) =3.994768602

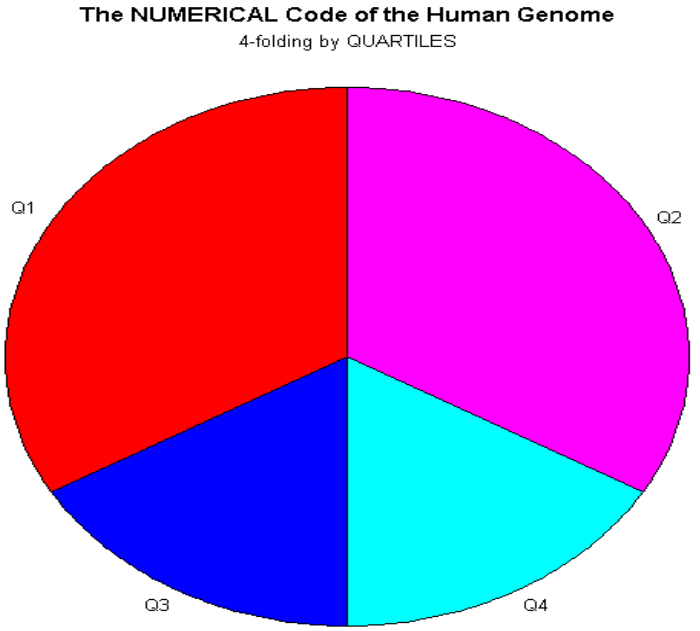
The Number « 5 » (Q1+Q2+Q3)÷(Q4) =4.996320389

The Number « 6 » (Q1+Q2+Q3+Q4)÷(Q4)=5.996320389

Other ratios : « 3/2 » etc.

(Q1+Q2+Q3+Q4)÷(Q1+Q2) =1.501043236





The perfect Whole Human Genome DNA ATOMIC WEIGHTS BALANCING...

A consequence of the « TWIN CODONS mirror symmetry » between codons is the PERFECT BALANCE between ATOMIC MASS of the 2 DNA STRANDS:

We prove that total atomic weights of each of the 2 simple DNA strands exhibit the same perfect symmetry: For the whole human genome, the balance ratio between both DNA strands is exactly = 1.000000456. Also, we noticed that this equilibrium has increased as the whole human genome sequence has grown in precision (successive releases of the draft human genomes sequences of April 2001, November 2002 and finally August 2003):

Balance mass strand1 / mass strand 2 evolution:

First Human Genome release April 2001: ***1.000039049***

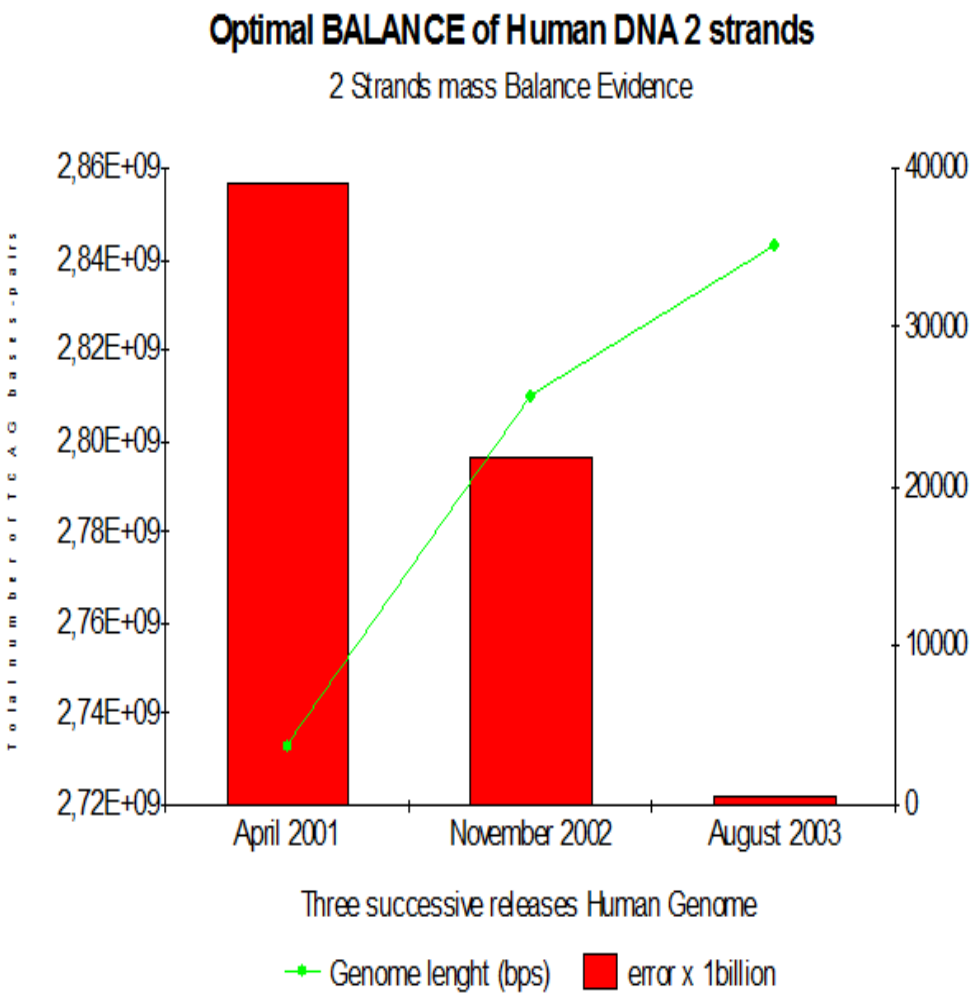
Intermediary release November 2002: ***1.000021780***

Finalized « BUILD34 » August 2003: ***1.000000456***

2 strands XX female whole genome: **1.000000599**

2 strands XY male whole genome: **1.000000309**

2 strands Hypothtical YY HumGMO genome: **1.000000005**



Perfect Whole Human Genome DNA CODON POPULATIONS, « Phi » the golden ratio and ATOMIC WEIGHTS BALANCING...

If we consider 2 clusters of 32 codon populations each, the most frequent (Q1+Q2) is exactly 2X as numerous as the least frequent of the 32 codons (Q3+Q4) . Exact ratio is 1.995859355...Then, what about TA versus CG quartiles composition?

Majors CG and TA: • T 1985989068 • C 857106311

• A 1982488350 • G 857309551

MAJOR CG = C+G = 1714415862 MAJOR TA = T+A = 3968477418

Minors CG and TA • T 537655334 • C 885972717

• A 536994232 • G 886719273

MINOR CG = C+G = 1772691990 MINOR TA = T+A = 1074649566

(MAJOR CG / MINOR CG) /'(MAJOR TA / MINOR TA) =

(MAJR CG x MINOR TA) / (MINOR CG x MAJOR TA) = **0.2618941805**

• (PHI*2) / 10 = 0.2618033989 **Error = 0.00009078157758**

OTHERS RATIOS/ NUMBER « 3 »: (Major CG / Major TA) + (Major CG / minor TA)

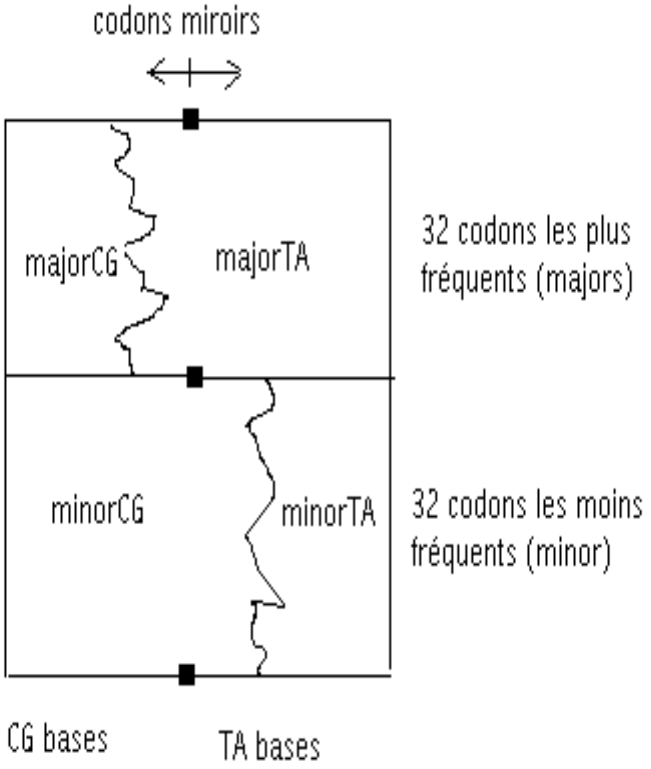
+ (Major CG / minor CG) = **3.002226104**

NUMBER « 3/2 »: (minor TA / Major TA) + (minor TA / Major CG)

+ (minor TA / minor CG) = **1.499096404**

NUMBER « 1 »:

(Major TA / Major CG) / minor CG = **0.9997090771**



(majorCG / minorCG) / (majorTA / minorTA) = Phi2/10

The perfect Whole Human Genome DNA CODON POPULATIONS, « Phi » the golden ratio and ATOMIC WEIGHTS BALANCING...

*2- ATOMIC WEIGHTS CODON POPULATIONS PERFECT BALANCING = Phi*2 / 10:*

- ***Base T : 125.105935*** - ***Base A : 134.119288***
- ***Base C : 110.094498*** - ***Base G : 150.118718***
- ***Majors 1 2***

MASSESTRAND1majCG 2.230608998E11

MASSESTRAND1majTA 5.143489452E11

- ***minors 3 4***

MASSESTRAND1minCG 2.30653882E11

MASSESTRAND1minTA 1.392851573E11

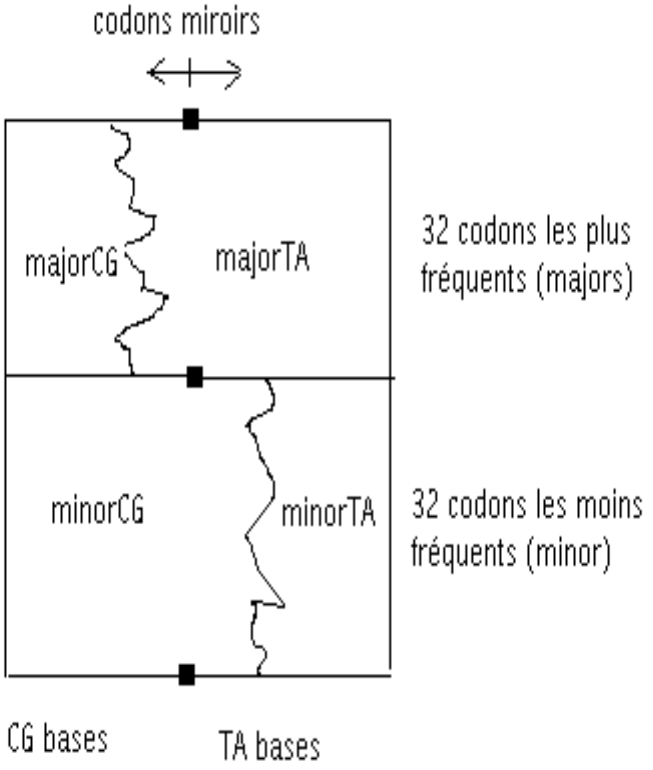
- ***(MASSESTRAND1majCG / MASSESTRAND1minCG)=0.9670806224***
- ***(MASSESTRAND1majTA / MASSESTRAND1minTA)=3.692776424***

(MASSESTRAND1majCG/ MASSESTRAND1minCG) / (MASSESTRAND1majTA / MASSESTRAND1minTA)

=0.2618844228

Error : 0.2618844228-(PHI2÷10) = 0.00008102388274.

Then an error of 81 millionths at whole human genome TCAG atomic weights balance



(majorCG / minorCG) / (majorTA / minorTA) = Phi2/10

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- Perspectives in Luc Montagnier's *« DNA Waves and Water »* breakthrough Luc Montagnier ,Lindau NOBELS conference, 28 June, 2010 - DNA BETWEEN PHYSICS AND BIOLOGY: « DNA WAVES AND WATER »

Perez JC. Interdiscip Sci. 2010 Sep;2(3):228-40. Epub 2010 Jul 25.
Codon populations in single-stranded whole human genome DNA Are fractal and fine-tuned by the Golden Ratio 1.618.

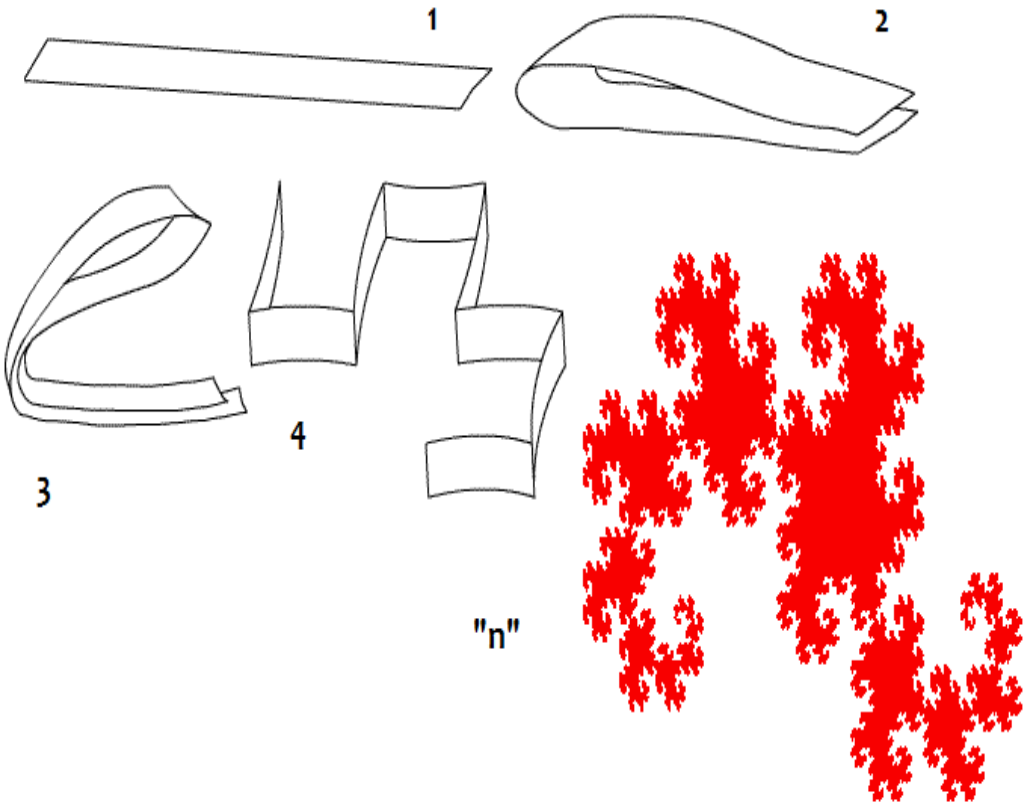
-I- ABSTRACT:

We propose a universal "Fractal Genome Code Law": The frequency of each of the 64 codons across the entire human genome is controlled by the codon's position in the Universal Genetic Code table. We analyze the frequency of distribution of the 64 codons (codon usage) within single-stranded DNA sequences. Concatenating 24 Human chromosomes, we show that the entire human genome employs the well known universal genetic code table as a *macro* structural model. The position of each codon within this table precisely dictates its population. So the Universal Genetic Code Table not only maps codons to amino acids, but serves as a global checksum matrix. Frequencies of the 64 codons in the whole human genome scale are a self-similar fractal expansion of the universal genetic code. Particularly, the 6 folding steps of codon populations modeled by the binary divisions of the ***"Dragon fractal paper folding curve"*** show evidence of 2 attractors. The numerical relationship between the attractors is derived from the Golden Ratio. We demonstrate that:

1. The whole Human Genome Structure uses the Universal Genetic Code Table as a tuning model. It predetermines global codons proportions and populations. The Universal Genetic Code Table governs both micro and macro behavior of the genome.

2. We extend the *Chargaff*'s second rule from the domain of single TCAG nucleotides to the larger domain of codon triplets.

3. Codon frequencies in the human genome are clustered around 2 fractal-like attractors, strongly linked to the golden ratio 1.618.



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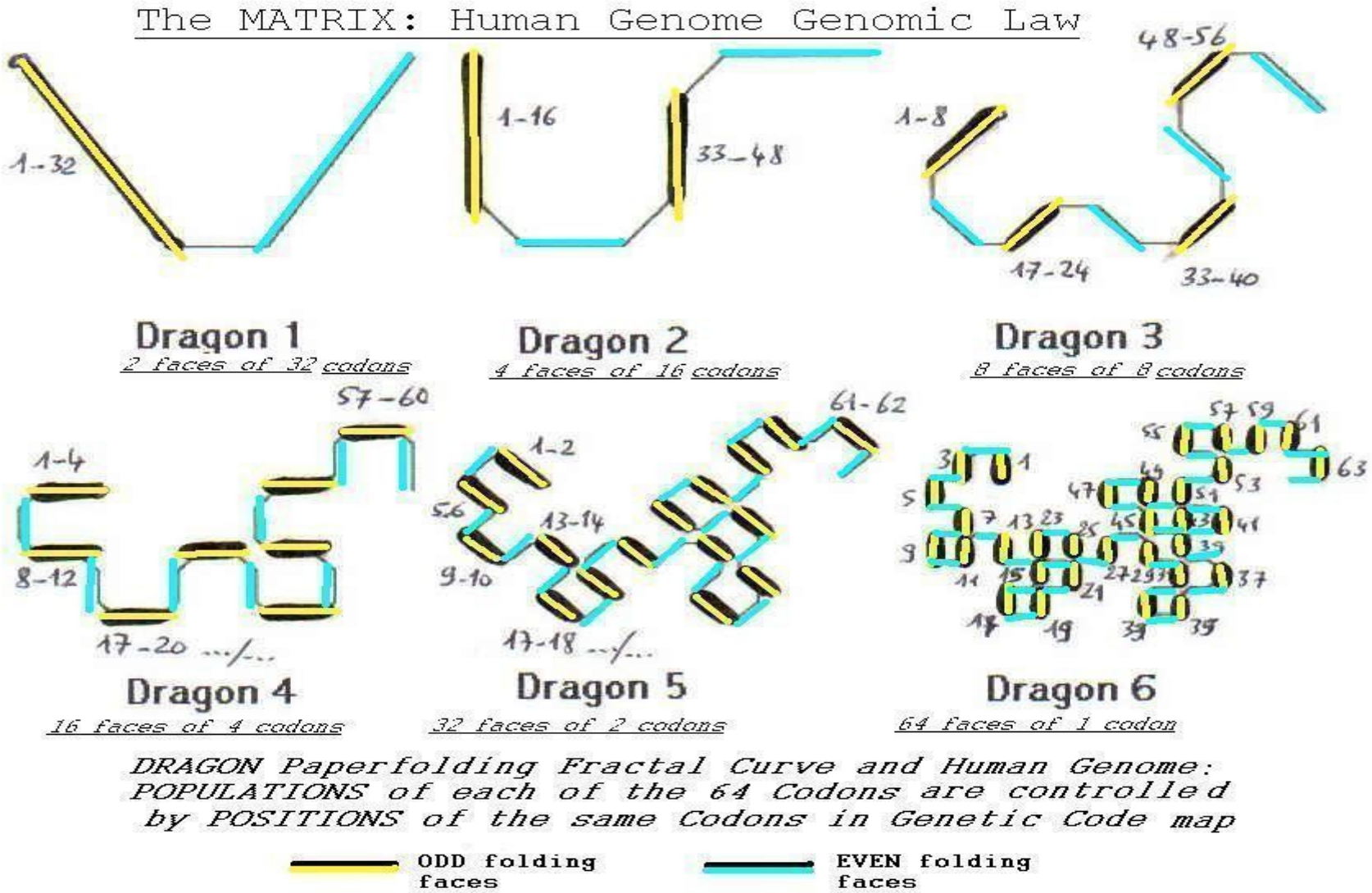
-II- RESHAPING THE GENETIC CODE TABLE BY FRACTAL DRAGON CURVE...



-III- Evidence of 2 « attractors »: « 1 » and « (3-Phi)/2 » where Phi = 1.618033 the Golden ratio

Table - Chessboard map summarizing major results, attractors and symmetries.

-I- 2 parts = 2*1 Dragon 1 2x32 Halves The ratio between the EVEN Half part and the ODD half part is

= 0.999247 = 1 (error=0.000753)

-II- 4 parts = 4*1 Dragon 2 4x16 Quartiles The ratio between EVEN Quartiles and ODD Quartiles is

= 0.691457 = (3 – Phi) / 2 (error=0.000474)

-III- 8 parts = 2*3 Dragon 3 8x8 Octants The ratio between EVEN Octants and ODD Octants is

= 0.999248 = 1 (error=0.000752)

-IV- 16 parts = 4*2 Dragon 4 16x4 Squares The ratio between EVEN Squares and ODD Squares is

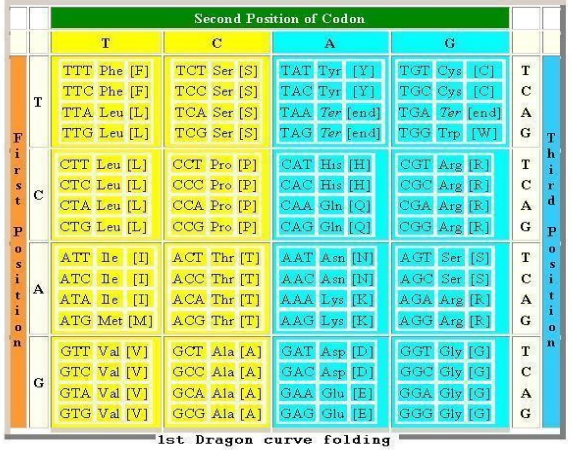
= 0.691458 = (3 – Phi) / 2 (error=0.000475)

-V- 32 parts = 2*5 Dragon 5 32x2 Binomes The ratio between EVEN Binomes and ODD Binomes is

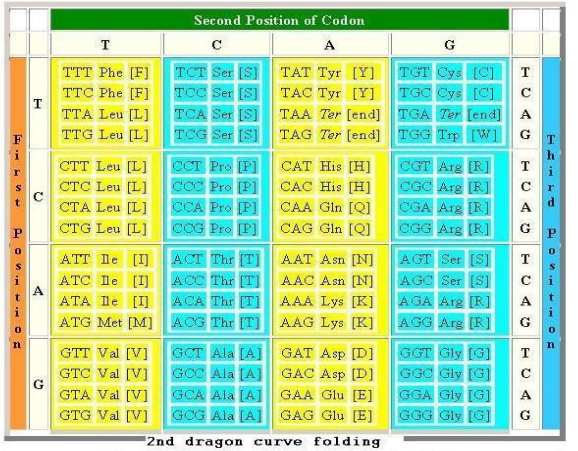
= 0.999247 =1 (error=0.000753)

-VI- 64 parts = 4*3 Dragon 6 64x1 codons The ratio between EVEN Codons and ODD Codons is

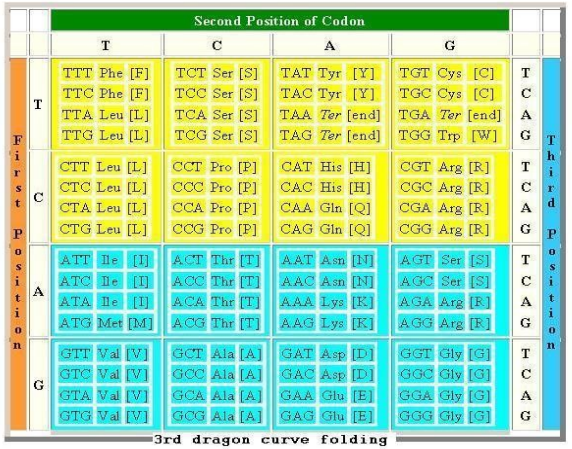
= 0.691458 = (3 – Phi) / 2 (error=0.000474)



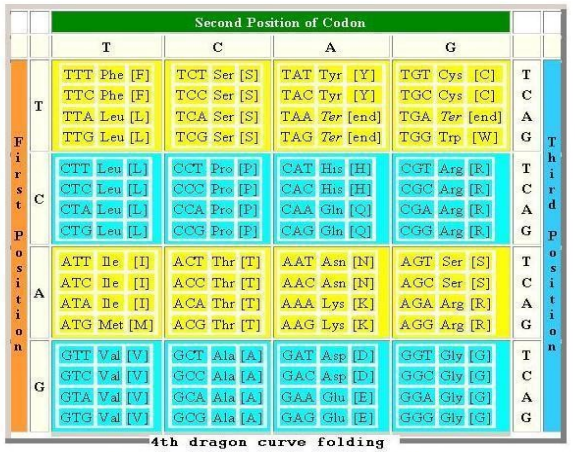
Dragon 1: ratio Dark/Light = 1



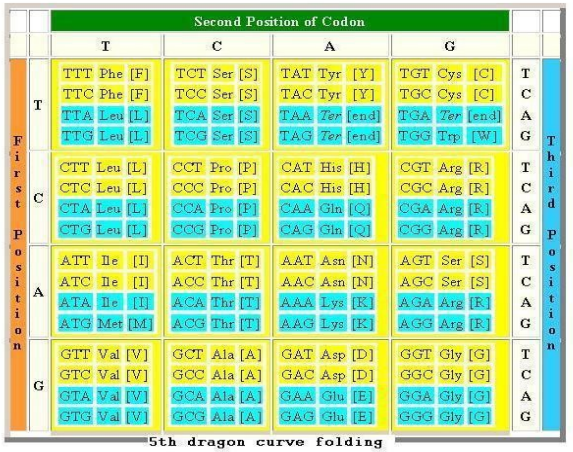
Dragon 2: ratio Dark/Light = (3 - Phi) / 2



Dragon 3: ratio Dark/Light = 1

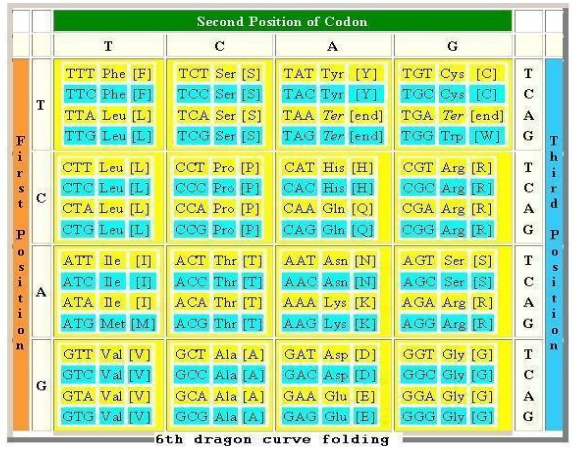


Dragon 4: ratio Dark/Light = (3 - Phi) / 2



Dragon 5: ratio Dark/Light = 1

"1" Attractor: "Odd" Folding



Dragon 6: ratio Dark/Light = (3 - Phi) / 2

"(3 - Phi) / 2" Attractor: "Even" Folding

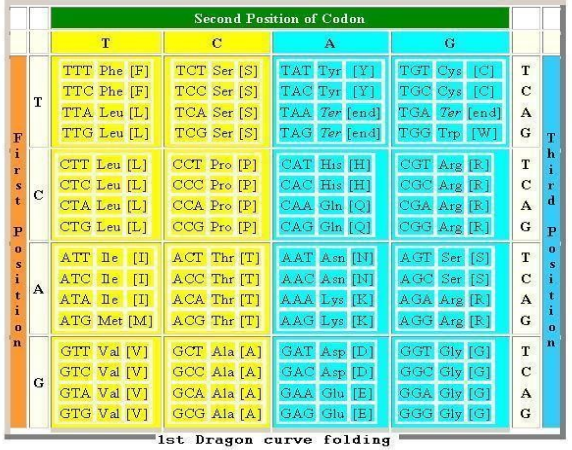
-IV- Extending 2 « attractors »: « 1 » and « (3-Phi)/2 »T+A and C+G nucleotides proportions

However, the most remarkable fact is the presence of both attractors «(3-Phi)/ 2» and «1» at the global T C A G nucleotide scale.

Effectively, attractor «1» corresponds to *Chargaff*'s second rule T=A and C=G which we have just demonstrated here.

The second attractor «(3-Phi)/2» is seen when we compute ratios T/C=1.447808424, A/G=1.444633555 and (T+A)/(C+G)=1.446220557.

When you compare these results with those of CODON POPULATIONS, they are extremely close to the ideal value 2 / (3-Phi) =1.447213595.



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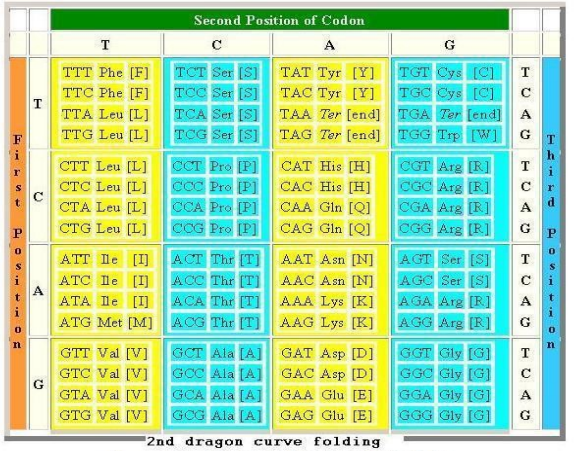
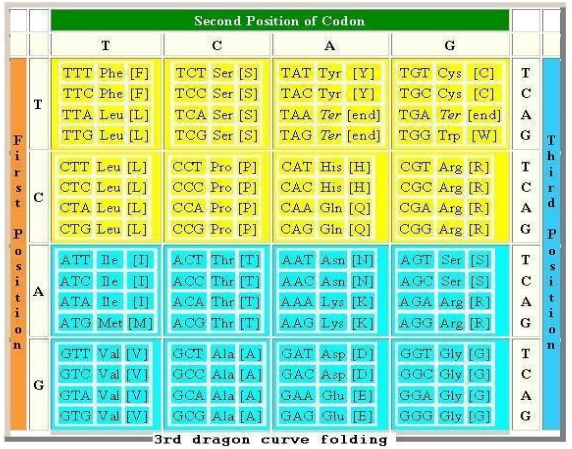
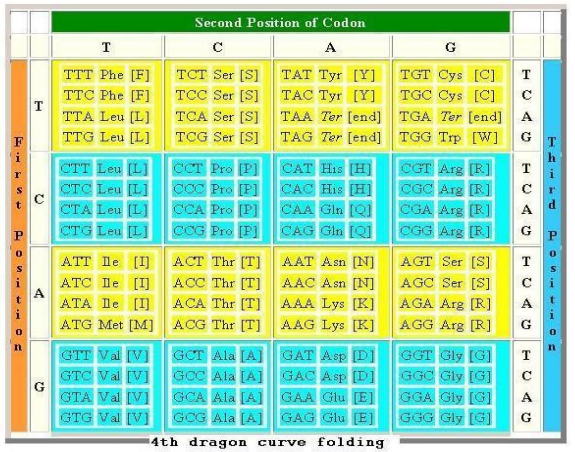


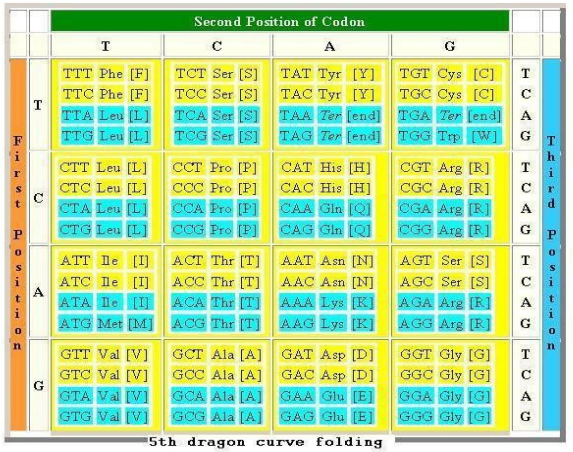
Dragon 2: ratio Dark/Light = (3 - Phi) / 2



Dragon 3: ratio Dark/Light = 1

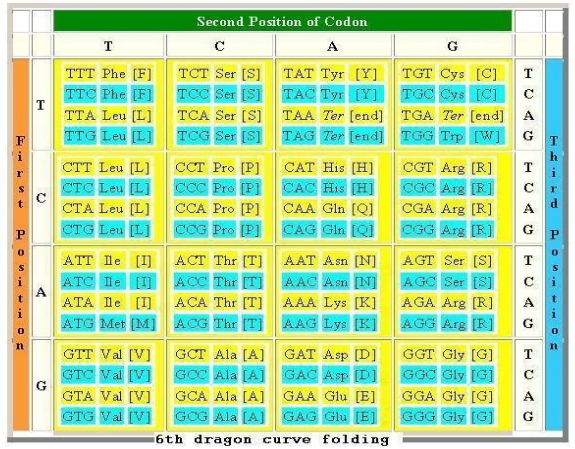


Dragon 4: ratio Dark/Light = (3 - Phi) / 2



Dragon 5: ratio Dark/Light = 1

"1" Attractor: "Odd" Folding



Dragon 6: ratio Dark/Light = (3 - Phi) / 2

"(3 - Phi) / 2" Attractor: "Even" Folding

-V- Towards a codon level generalization of *Chargaff*'s second rule.

Chargaff's second parity rule appears to be extended from the nucleotide-level to populations of codon triplets, in the case of whole single-stranded Human genome DNA.
A kind of "codon-level second Chargaff's parity rule" is proposed as follows:

Codon populations where 1st base position is T are identical to codon populations where 3rd base position is A:
« % codons Twx ~ % codons yzA » (where Twx and yzA are mirror codons i.e TCG and CGA).
Codon populations where 1st base position is C are identical to codon populations where 3rd base position is G:
« % codons Cwx ~ % codons yzG » (where Cwx and yzG are mirror codons i.e CTA and TAG).
Codon populations where 2nd base position is T are identical to codon populations where 2nd base position is A:
« % codons wTx ~ % codons yAz » (where wTx and yAz are mirror codons i.e CTG and CAG).
Codon populations where 2nd base position is C are identical to codon populations where 2nd base position is G:
« % codons wCx ~ % codons yGz » (where wCx and yGz are mirror codons i.e TCT and AGA).
Codon populations where 3rd base position is T are identical to codon populations where 1st base position is A:
« % codons wxT ~ % codons Ayz » (where wxT and Ayz are mirror codons i.e CTT and AAG).
Codon populations where 3rd base position is C are identical to codon populations where 1st base position is G:
« % codons wxC ~ % codons Gyz » (where wxC and Gyz are mirror codons i.e GGC and GCC).

WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

-I- Summary:

- Now we run individually on the single stranded DNA of each human genome chromosome the same analysis described in *"DRAGON fractal paper folding curve"* fine-tuned around the ***"Golden ratio"*** (*"Codon Populations in single-stranded DNA Whole Human Genome Are fractal and fine-tuned by the Golden Ratio 1618"* , 2010, Interdisciplinary Science).
- We recall that ATTRACTOR « 1 » is provided by computing TC/AG bases populations.
- Exp: 1st codons reading frame:

T= 841214808 C=581026325 A=839827524 G=581342944

(T+A)÷(C+G)

1.446220557

(T+C)÷(A+G)

1.000753368

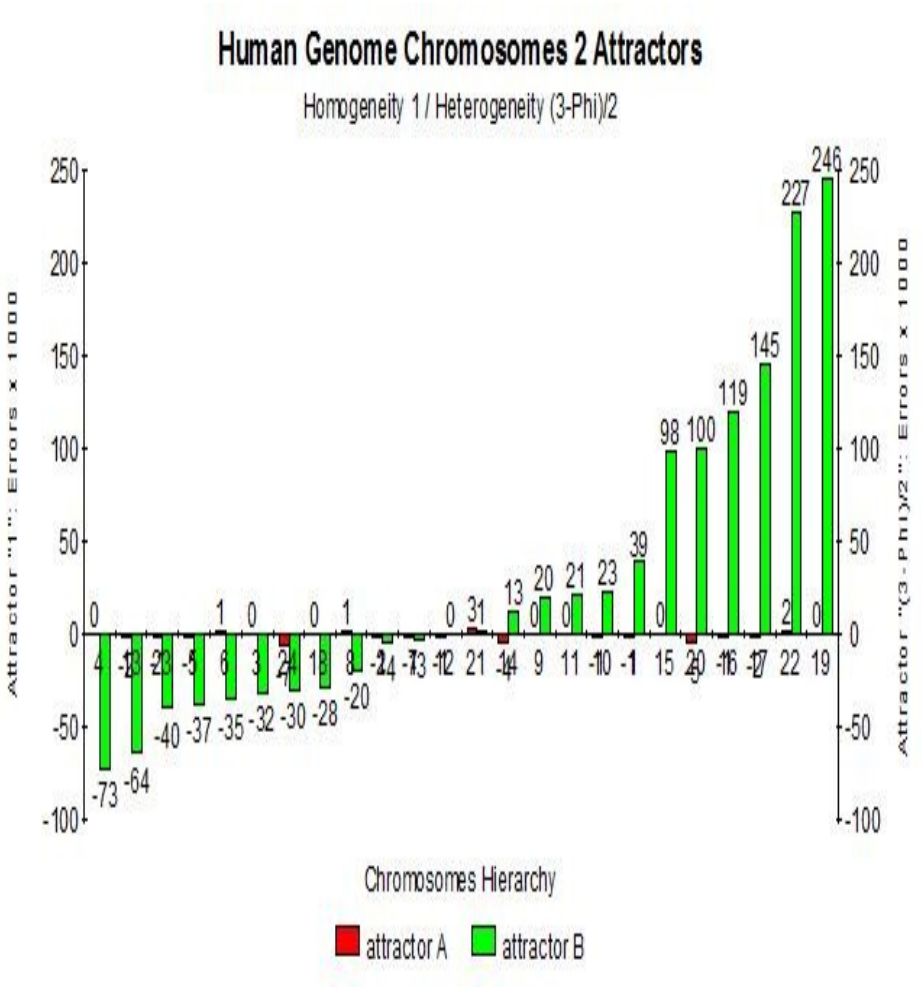
•And ATTRACTOR « (3-Phi)/2 » is provided by computing TA/CG bases populations.

•

•Curiously the « 1 » attractor is homogeneous and conserved in the case of the 24 chromosomes.

•

•Contrarly, the « (3-Phi)/2 » appears to be highly heterogeneous.



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-II- Results:

ANALYSING CODON POPULATIONS – Generalizing
Attractors « 1 » and « (3-Phi)/2 » from whole human génome to the
24 individual chromosomes:

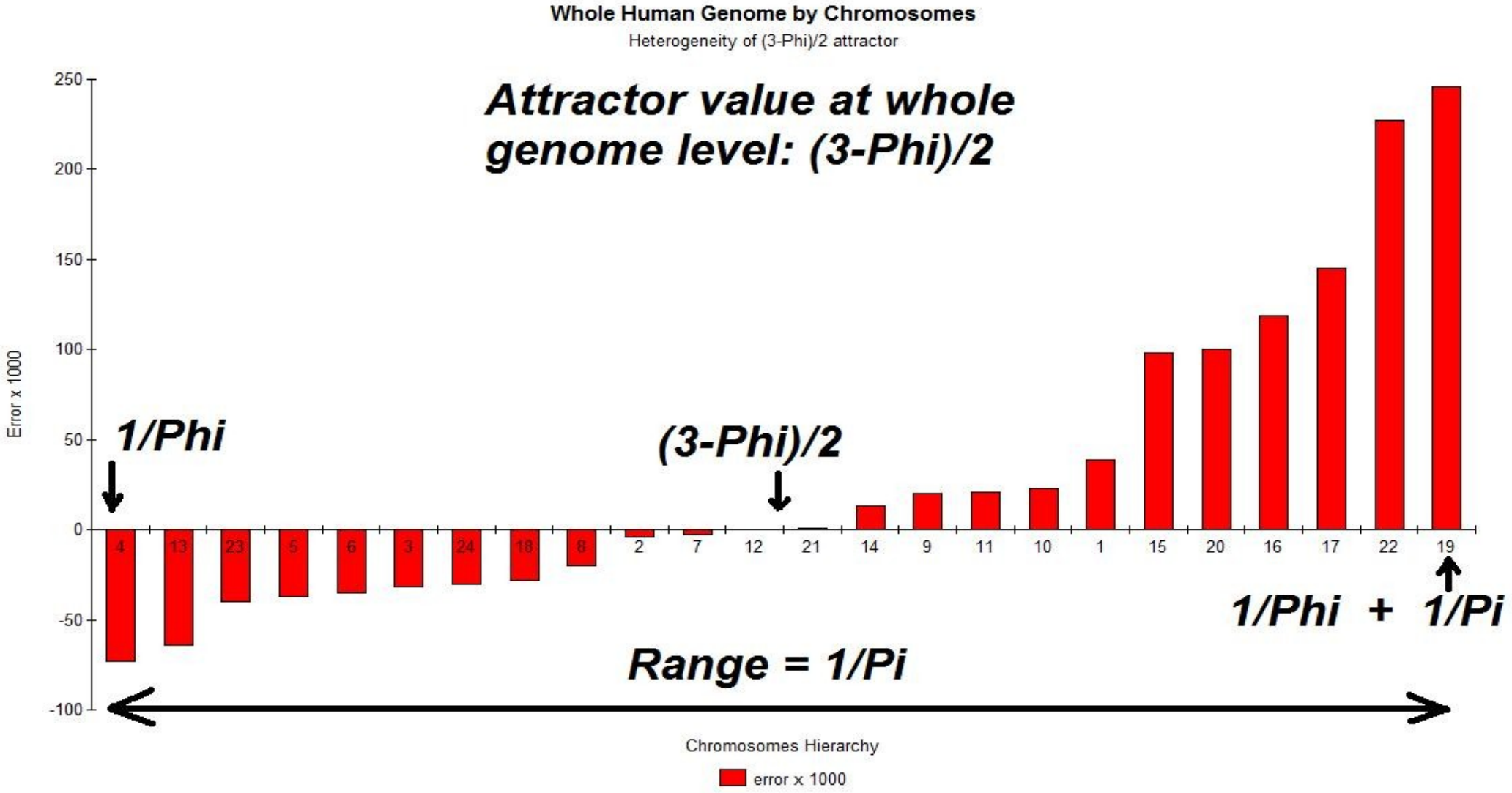
CHROMOSOME / 6 cases: dragon1 to dragon6 / The 2 ERRORS vs attractors « 1 »(dragon1) and « (3-Phi)/ 2 » (dragon2)

4 0.9998414507 0.6182846465 0.9998417076 0.6182848147 0.999841258 0.6182847866 **-0.0001585493105 -0.07269835919**
13 0.9982668844 0.6265479796 0.9982671351 0.6265483118 0.9982668008 0.6265479242 -0.001733115626 -0.06443502604
23 0.9985556692 0.6514329116 0.998556044 0.6514330944 0.9985553212 0.6514331675 -0.00144433077 -0.03955009401
5 0.9989193956 0.6538648891 0.9989195307 0.6538649353 0.9989193056 0.6538649507 -0.001080604355 -0.03711811656
6 1.000525858 0.6555684149 1.000526217 0.6555686115 1.000525762 0.6555683821 0.0005258577024 -0.03541459078
3 0.9997091032 0.6580066635 0.9997092677 0.65800672 0.9997090621 0.6580067483 -0.0002908967547 -0.03297634215
24 0.9931744751 0.6591081629 0.9931764092 0.6591089446 0.9931727023 0.6591088329 -0.00682552488 -0.03187484278
18 1.000012833 0.6607156383 1.000013101 0.66071586 1.000012833 0.6607156753 0.00001283261832 -0.03026736733
8 1.000720369 0.6709809502 1.00072065 0.670981166 1.000720116 0.6709810875 0.000720368643 -0.02000205546
2 0.9990576615 0.6729417129 0.9990578802 0.6729418778 0.9990572914 0.6729417246 -0.000942338463 -0.01804129279
7 0.9988696848 0.6866614322 0.9988699173 0.6866616713 0.9988693231 0.6866615793 -0.001130315215 -0.004321573483
12 **0.999372296 0.688058808 0.9993724808** 0.6880586324 0.9993719881 0.6880589617 **-0.000627703979 -0.002924197639**
21 1.003369337 0.6914042722 1.003369337 0.6914041879 1.003369337 0.6914045252 0.003369336504 0.0004212665743
14 0.9963855347 0.6915117446 0.9963856261 0.6915117118 0.996385489 0.6915116133 -0.00361446528 0.0005287389482
9 0.9999354134 0.7037292009 0.9999365895 0.7037303055 0.9999341334 0.7037302302 -0.00006458664014 0.01274619523
11 1.000343902 0.7112162565 1.000343993 0.7112164354 1.000343474 0.7112165025 0.0003439015863 0.02023325083
10 0.9992210126 0.7116203869 0.9992218353 0.7116209006 0.9992204032 0.71162099 -0.000778987353 0.02063738129
1 0.9988587539 0.7144457101 0.9988596375 0.714446307 0.998857708 0.7144462407 -0.001141246105 0.02346270441
15 1.000152264 0.7302638674 1.000152806 0.7302640148 1.000151624 0.7302641622 0.0001522643938 0.03928086178
20 0.994565246 0.7893931557 0.9945655138 0.7893936406 0.9945649782 0.7893933712 -0.005434753969 0.09841015006
16 0.9986619885 0.8100695879 0.9986625382 0.8100697109 0.9986616887 0.8100699568 -0.001338011494 0.1190865823
17 0.9980299988 0.8357433305 0.9980305641 0.8357437209 0.9980295363 0.8357436341 -0.001970001184 0.1447603248
22 1.002325596 0.917982601 1.002326646 0.9179838861 1.002324429 0.9179833506 0.002325595764 0.2269995954
19 0.9997711858 0.9366474189 0.9997715443 0.9366476878 0.9997710425 0.9366478223 **-0.0002288141751 0.2456644133**

WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

Analysing Attractor « (3-Phi)/ 2 » reveals HETEROGENEITY, SYMMETRY and NUMERICAL л and ф STRUCTURES

-III- Chromosomes numerical network classification scale: Evidence of 2 limits: 1/ Phi (chr4) and (1/ Phi + 1/ Pi) chr19.



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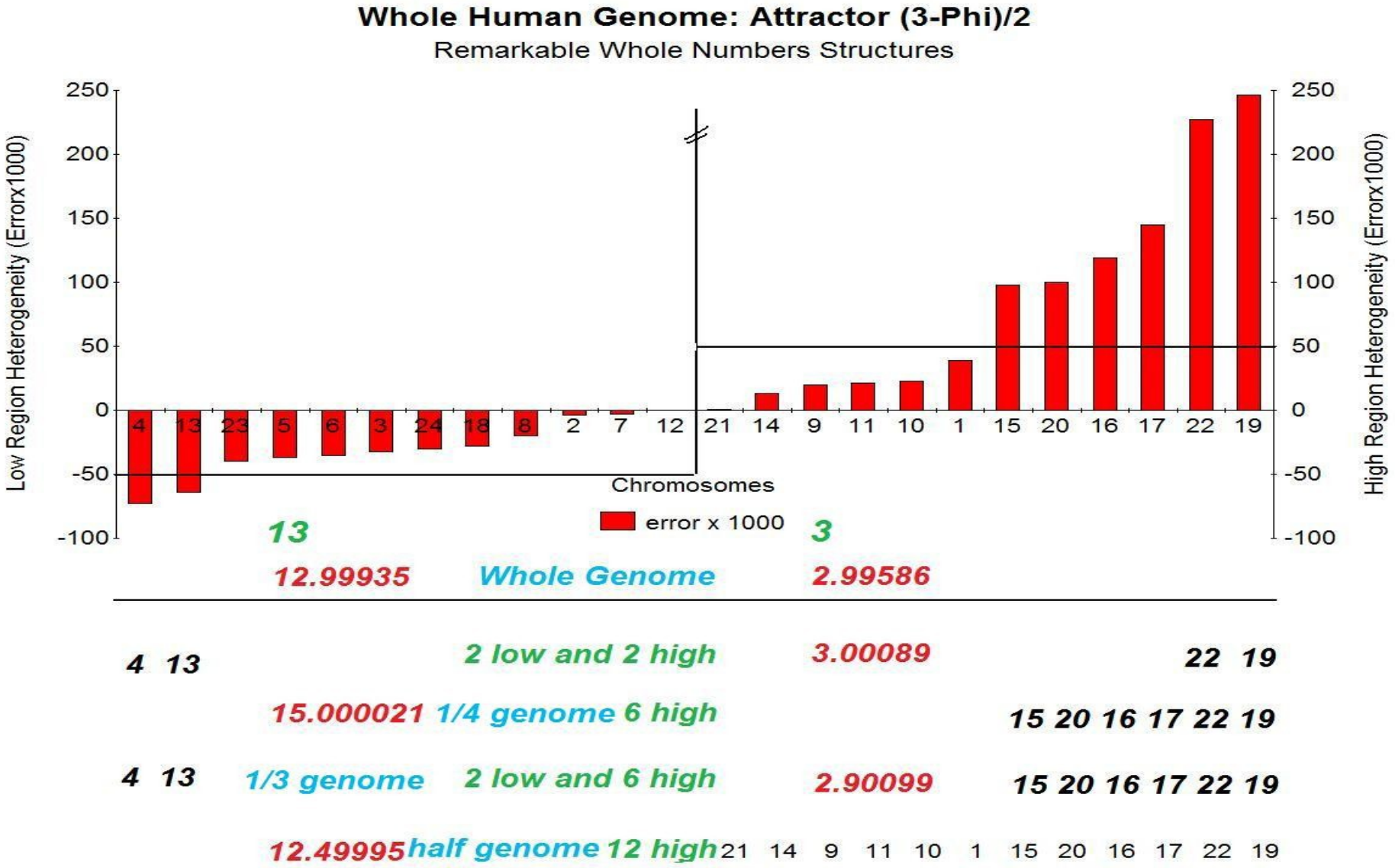
Chromosome	Remarkable value	Ideal Real value	Measured Real value	Error
Low level: chromosome: 4	1/Phi	0.6180339887	0.6182846465	0.0002506578
Medium level chromosome 12	(3-Phi)/2	0.6909830056	0.6914042722	0.0004212666
WHOLE GENOME	(3-Phi)/2	0.6909830056	0.6914573163	0.0004743107
Medium level chromosome 21	(3-Phi)/2	0.6909830056	0.6915117446	0.000528739
High level: chromosome: 19	1/Phi + 1/Pi	0.9363438749	0.9366474189	¯0.000303544
Scope of variability	1/Pi	0.3183098862	0.3183627724	¯0.0000528862

Analysing Attractor « (3-Phi)/ 2 » reveals HETEROGENEITY, SYMMETRY and NUMERICAL л and Ф STRUCTURES

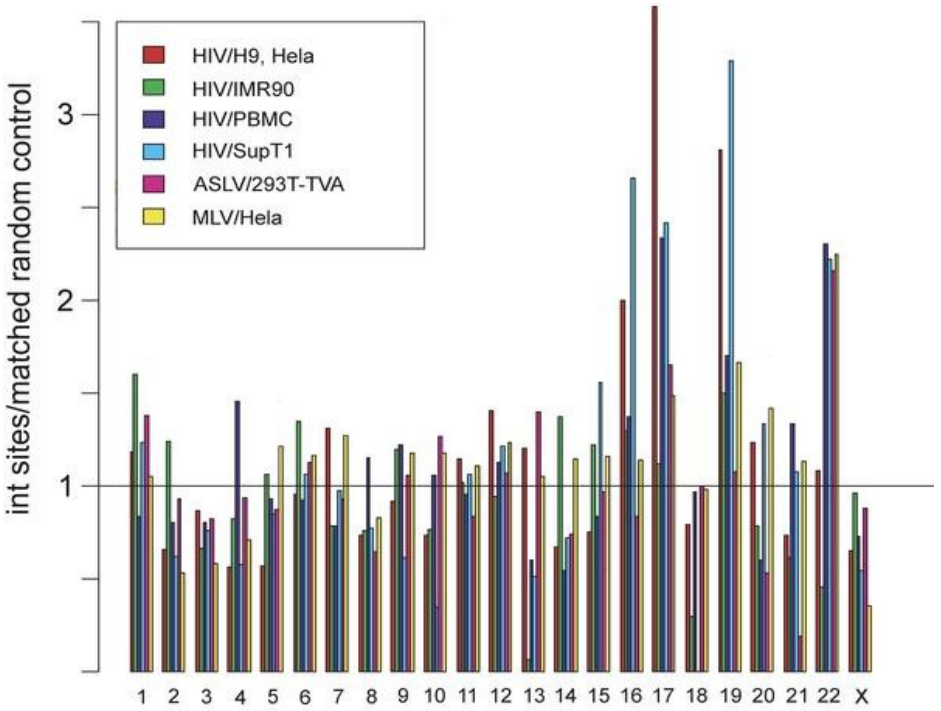
-IV- Chromosomes network classification scale: STRUCTURE CHARACTERIZATION.

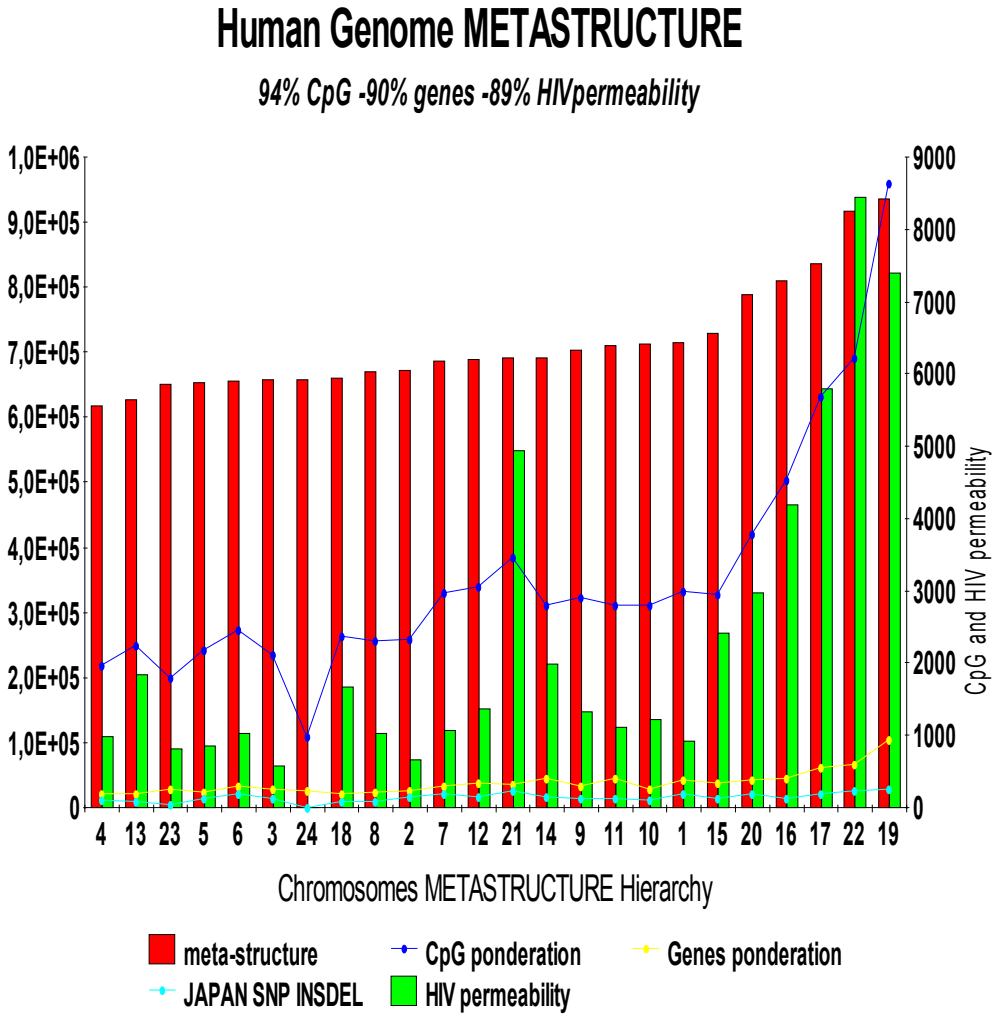


WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

-V- CHROMOSOMES META-STRUCTURE IS 89% CORRELATED WITH CHROMOSOMES PERMEABILITY TO INTRUSION OF RETROVIRUSES...

A functionality of this fine-tuned structure appears: the structure is **90%** correlated with the density of genes per chromosome from the Human Genome project. It is **89%** correlated with the chromosome's permeability to intrusion by retroviruses like HIV, **94%** with CpG density Mitchell et al 1. Mitchell RS, Beitzel BF, Schroder AR, Shinn P, Chen H, et al. (2004) Retroviral DNA Integration :ASLV, HIV, and MLV Show Distinct Target Site Preferences. PLoS Biol 2(8) : e234.



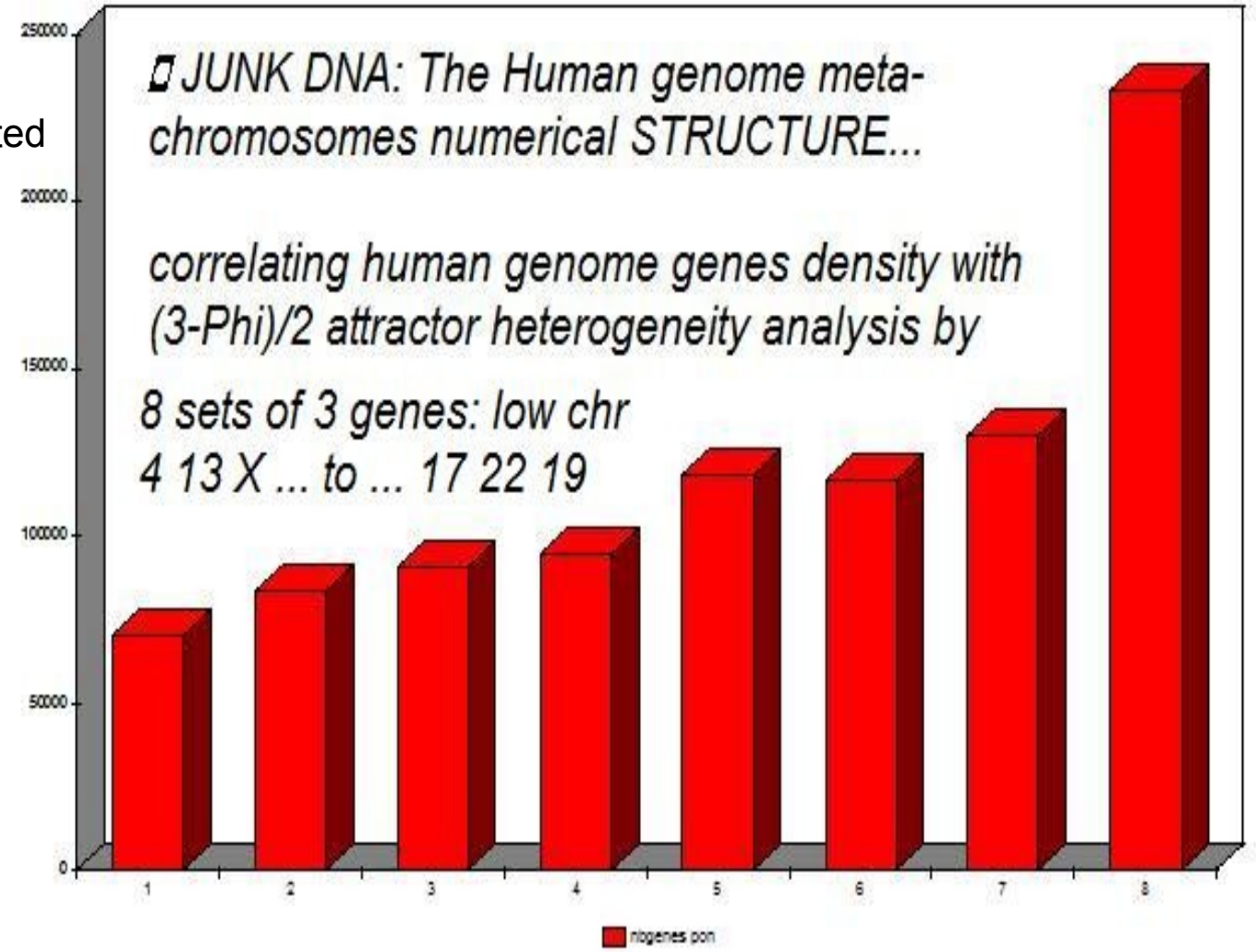


WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

-VI- CHROMOSOMES META-STRUCTURE IS 90% CORRELATED WITH GENES DENSITY BY CHROMOSOMES (HUMAN GENOME PROJECT)..

A functionality of this fine-tuned structure appears:

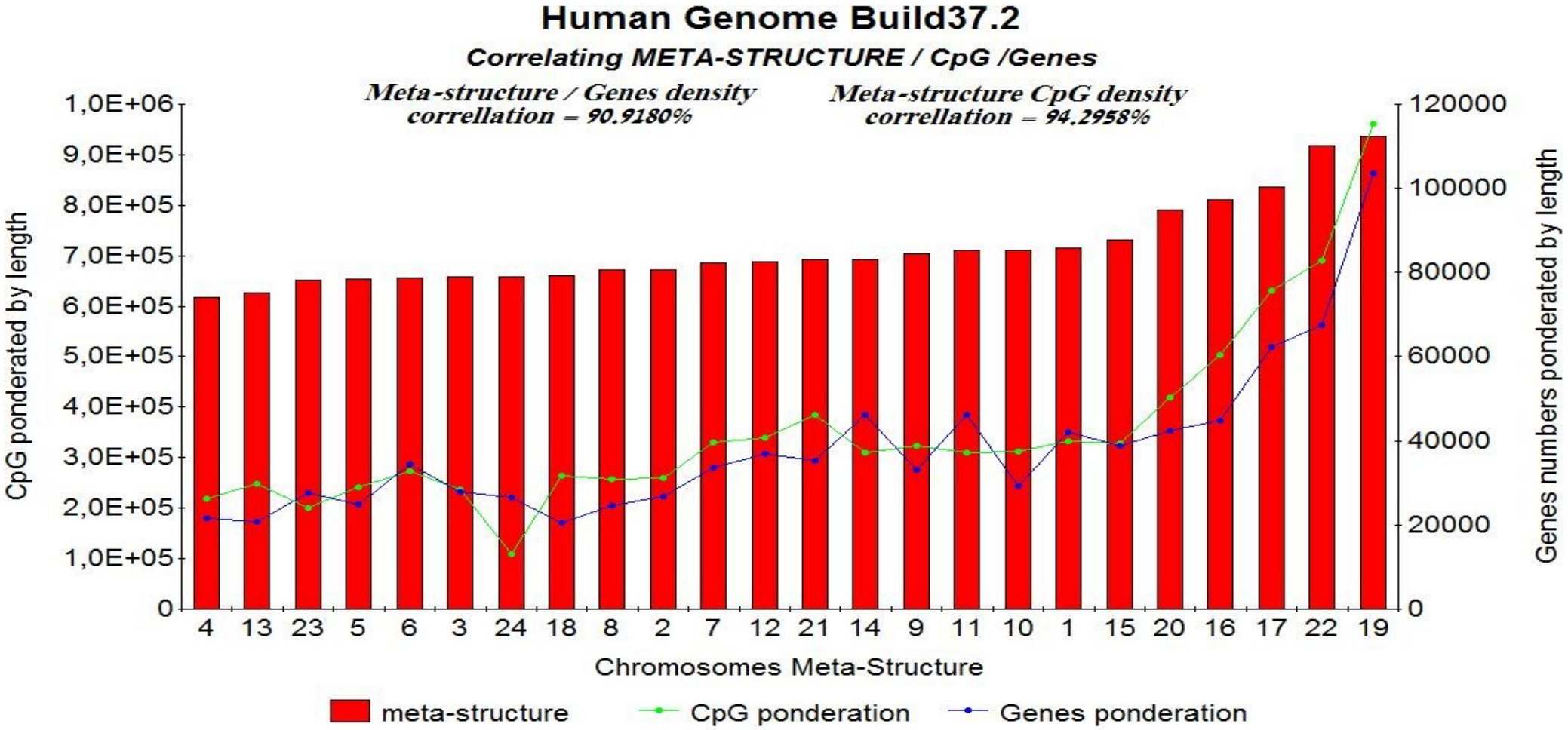
the structure is **90.91%** correlated with the density of genes per chromosome from the Human Genome project.



WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

-VII- CHROMOSOMES META-STRUCTURE IS 94% CORRELATED WITH CpG DENSITY BY CHROMOSOMES ...

A functionality of this fine-tuned structure appears: the structure is **90%** correlated with the density of genes per chromosome from the Human Genome project. It is **89%** correlated with the chromosome's permeability to intrusion by retroviruses like HIV, **94%** with CpG density



WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS
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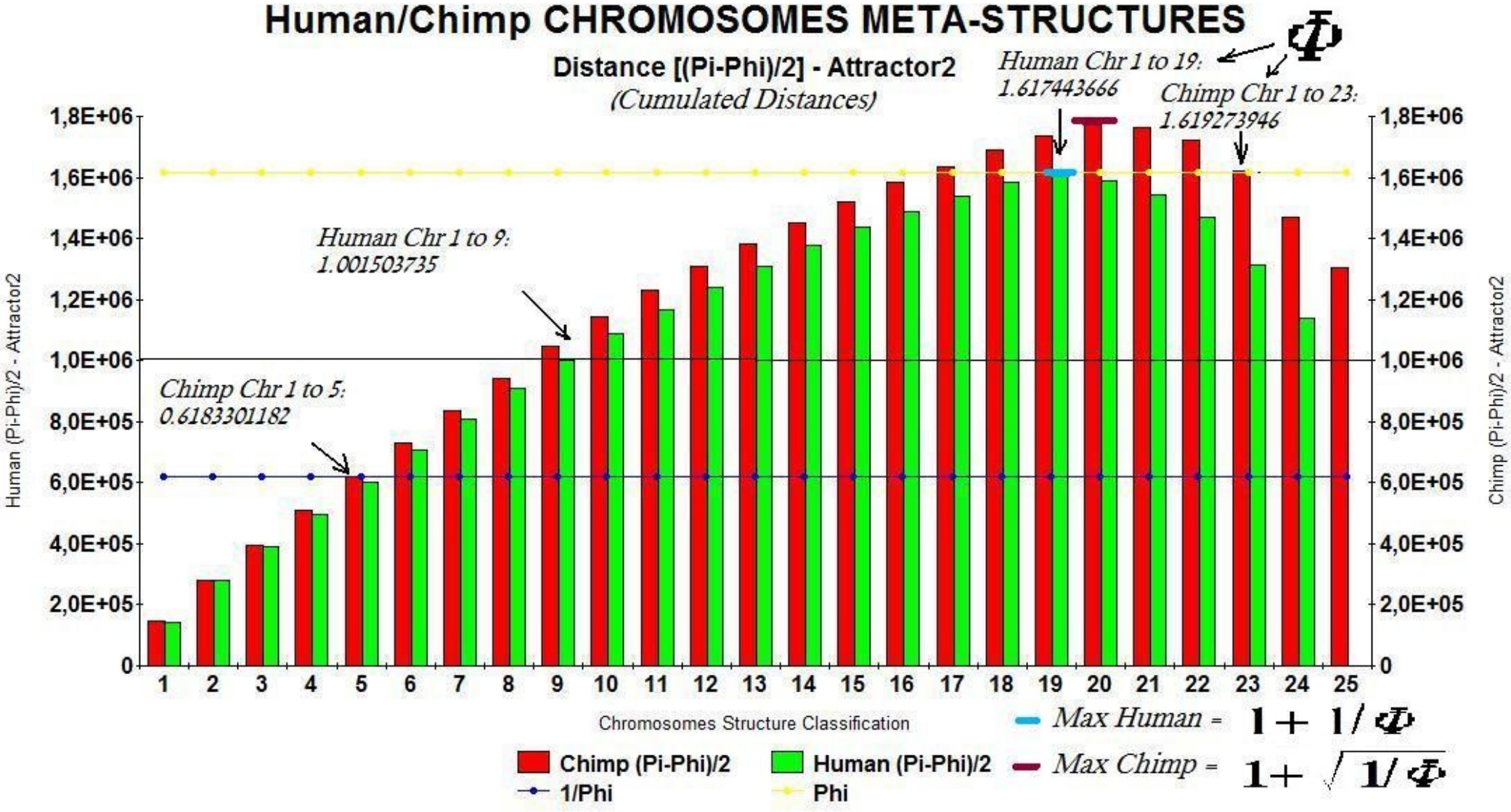
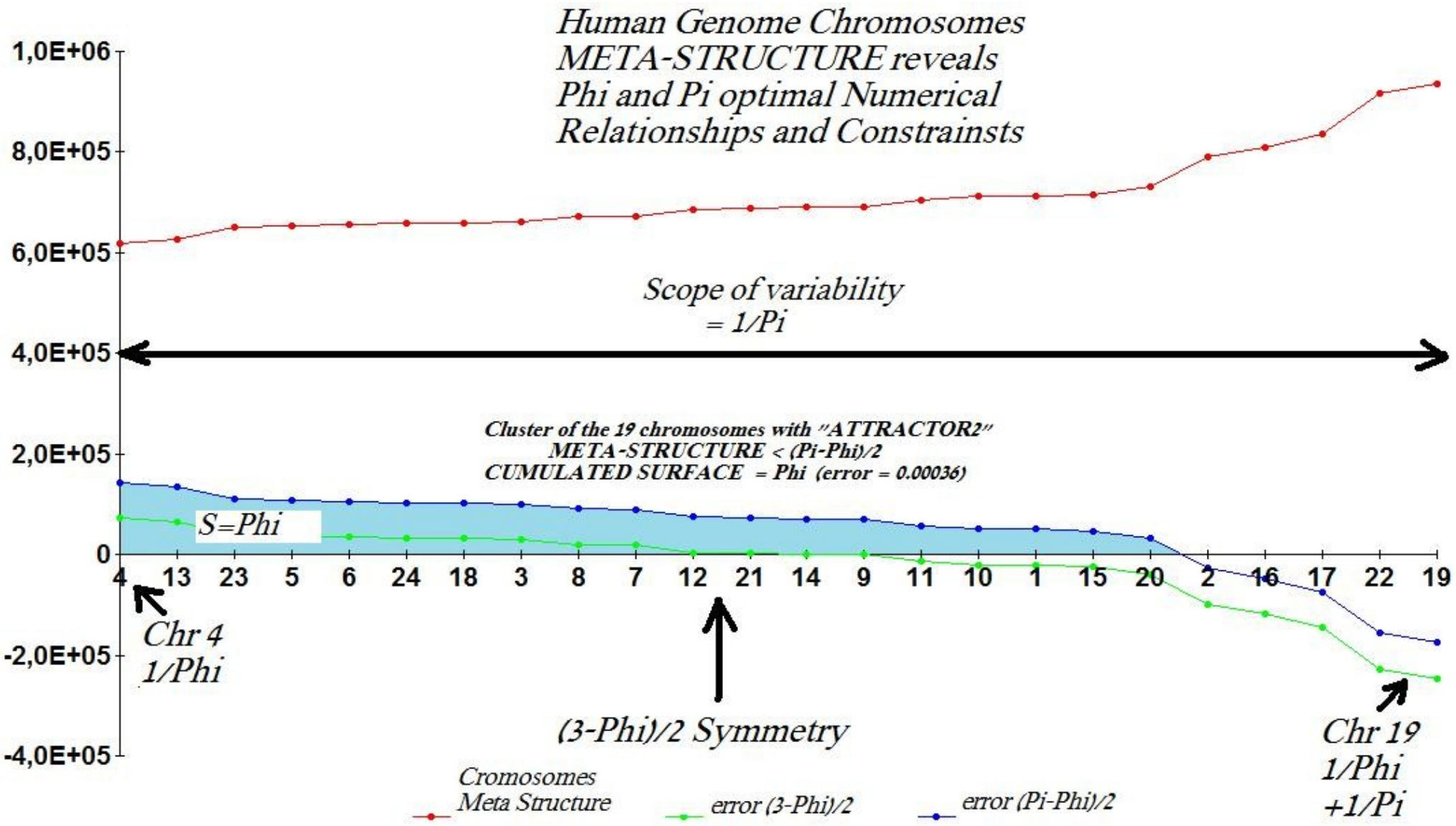
-VIII- « INTEGRATING » the meta strucure (cumulating distances) reveals a maximum=Phi (1.618)... in both cases of HUMAN and CHIMP genomes!



WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф…

-IX- « 2 order INTEGRATION » of the meta strucure (re-cumulating cumulated distances) reveals a Surface of integration=Phi (1.618)…



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- **Part I - BACKGROUND:**
- DNA supracode (1991-1997)
- Human genome Codon populations: Numbers and atomic weighs perfect balancing (2009)
- **Part II - RESULTS:**
- Whole Human Genome Codon Populations reveals central rôle of « Phi » the « Golden ratio » J.C. Perez - Interdiscip Sci Comput Life Sci (2010) 2: 1–13 DOI: 10.1007/s12539-010-0022-0« Codon Populations in Single-stranded Whole Human Genome DNA Are Fractal and Fine-tuned by the Golden Ratio 1.618 »
- Proof of a Functional Human Chromosomes Meta-structure involving « Pi » and « Phi » Universal Constants.
- **Part III - FUTURES:**
- **The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes: Binary Code and Waveforms in DNA...** ***« Is there an Equation for Life »?***
- **Perspectives in Luc Montagnier's** ***« DNA Waves and Water »*** **breakthrough Luc Montagnier ,Lindau NOBELS conference, 28 June, 2010 - DNA BETWEEN PHYSICS AND BIOLOGY: « DNA WAVES AND WATER »**

$$\text{Proj}\,(m) = [\ 1 - [\ 4\pi\sqrt{\varphi}\varphi\varphi^2\ ]\ ]\ m$$

with: $\sqrt{\varphi}=1/\sqrt{\Phi}$ *Phi is the GOLDEN RATIO* Φ

$\varphi = 1/\Phi$

$\varphi^2 = 1/\Phi^2$

- **The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:**

TIME – I - PROJECTION - First Law: Law of CODIFICATION and UNIFICATION of all GENETIC information: bioatoms, DNA, RNA and amino acids

$$\text{Proj}(m) = [\ 1 - [\ 4\pi\sqrt{\varphi}\varphi\varphi^2\ ]\ ]\ m$$

with: $\sqrt{\varphi} = 1/\sqrt{\Phi}$ Phi is the GOLDEN RATIO Φ

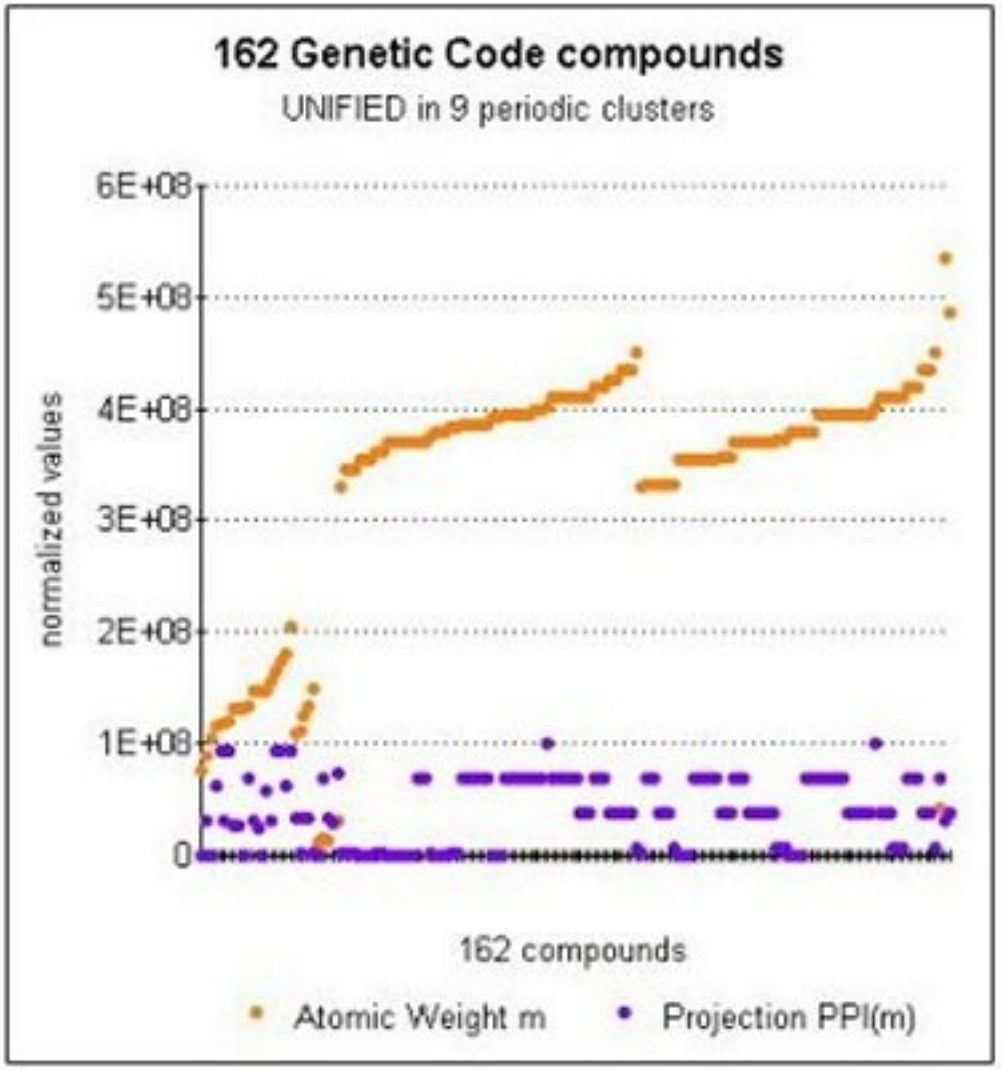
$\varphi = 1/\Phi$

$\varphi^2 = 1/\Phi^2$

- Between 1997 and 2003, we discovered then explored this universal formula of numerical projection of any biologcal material atomic weight.
- From the result of the projection, we keep only the decimal residue.
- Then, applying this formula to various biological components we discovered that all projections are close multiples of Pi/10=0.314...=18°
- Now we could associate with any projection an integer number « n » as proj(component) = « n » Pi/10 where n is in the range [-10,+10]
- Examples:
- Atomic weight of GLY = 75.067542.
- projection (GLY) = 0.0001271351803.
- Close Angle N.PI/10 =: 0.000000000 (N=0).
- Approximation error : (GLY,0) = 0.0001271351803.
- PI-MASS(GLY) = 0 or 0° or also 0.Pi/10.
- Others Pi-Mass: Carbon=0 Pi/10, Hydrogen=-1 Pi/10
- Oxygen= -1 Pi/10, Nitrogen=+2 Pi/10 GGG base= -3 Pi/10
- Lys amino acid=+4 Pi/10, GGU codon RNA =-2 Pi/10 etc...

- **The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:**

TIME -II- PULSATION. First Law: Law of CODIFICATION and UNIFICATION of all GENETIC information: bioatoms, DNA, RNA and amino acids



- Applying this Projection Coding Law to ALL BIOLOGICAL MATERIALS, we obtain a « barcode » like banding as follows...
- Here we analysed 162 compounds
- Of all usual genetic materials as 20 amino acids, 64 DNA codons, 64 RNA codons, 5 nucleotides TUCAG etc...
- In orange, the atomic weights, In purple, the integer numbers associated codes... doing a barcode like printing, showing evidence of the UNIFICATION in a COMMON CODE of all the 3 DNA, RNA and amino acids worlds.

- **The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:**

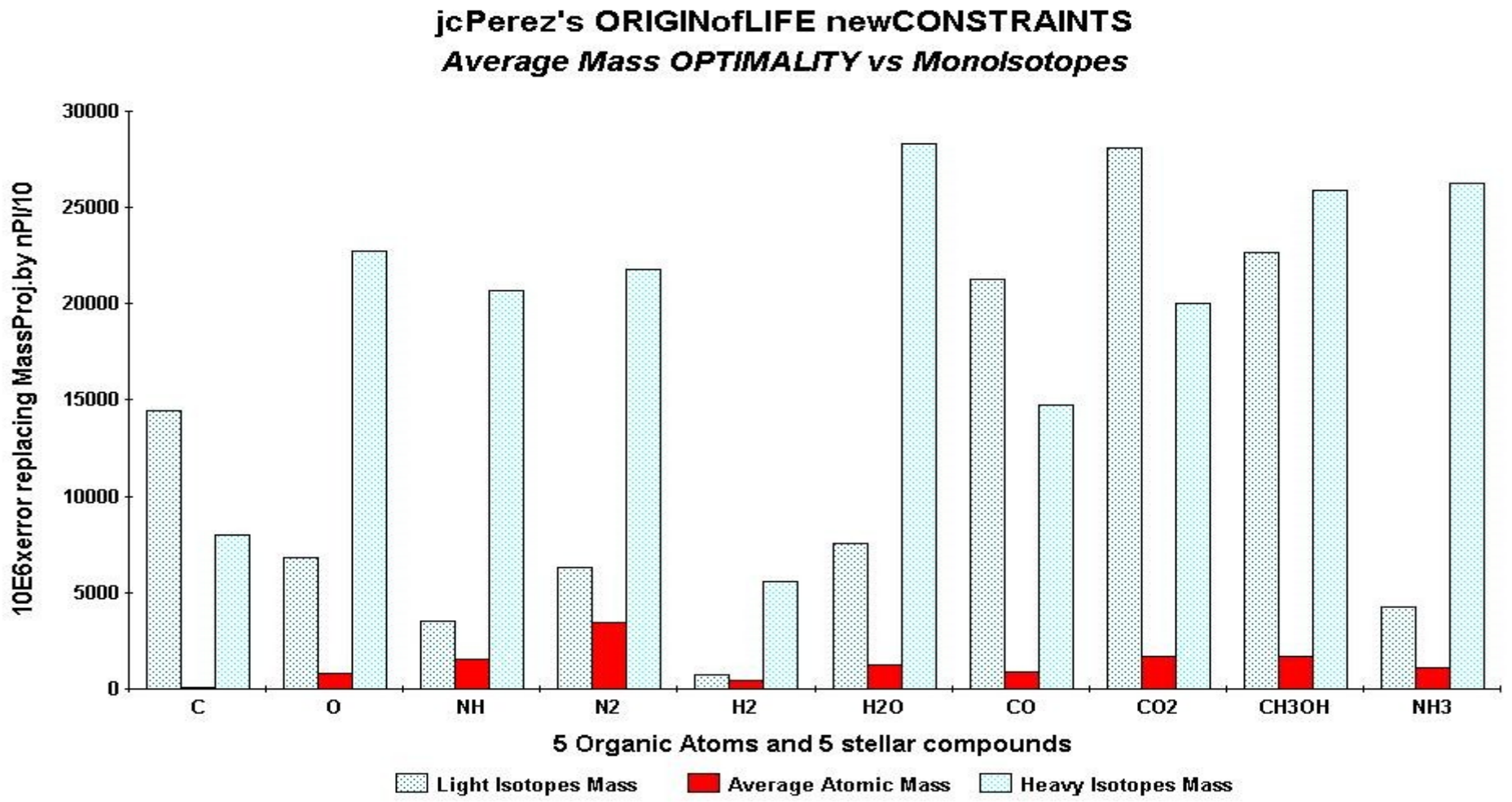
TIME -III- CODIFICATION. First Law: Law of CODIFICATION and UNIFICATION of all GENETIC information: bioatoms, DNA, RNA and amino acids

	-3 PI/10 et moins	-2 PI/10	-1 PI/10	0 PI/10	+1 PI/10	+2 PI/10	+3 PI/10	+4 PI/10	+5 et +7 PI/10
BIOATOMES	P(-4pi/10)		H O	C	N			S	
BASES				U G I	T C A				
ANNEXES		Ph/sucre ARN	CONH	H2O	CH2 Ph/sucre ADN				
ACIDES AMINES			Asp	Asn Glu Gly Ser	Ala Gln His Thr	Pro Tyr Cys (+2)	Arg Phe Trp Val	Ile Leu Lys Met (+4)	Cys (+5) Met (+7)
CODONS ADN	ggg	gtg gcg gag tgg cgg agg ggt ggc gga	ttg ctg atg gtt gtc gta tcg ccg acg gct gcc gca tag cag aag gat gac gaa tgt tgc tga cgt cgc cga agt agc aga	ttt ttc tta ctt ctc cta att atc ata tct tcc tca cct ccc cca act acc aca tat tac taa cat cac caa aat aac aaa					
CODONS ARN	uuu uug guu gug ugu ugg ggu ggg	uuc uua cuu cug auu aug guc gua ucu ucg gcu gcg uau uag gau gag ugc uga cgu cgg agu agg ggc gga	cuc cua auc aua ucc uca ccu ccg acu acg gcc gca uac uaa cau cag aau aag gac gaa cgc cga agc aga	ccc cca acc aca cac caa aac aaa					

The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:

TIME -IV- TUNING. *The optimized bio-atoms average atomic mass provides the perfect isotopes proportions balancing tuning of Life C O N H bio-atoms then of all DNA, RNA, amino acids components...*

In other words: PROJECTION law is OPTIMAL for AVERAGE ATOMIC WEIGHTS



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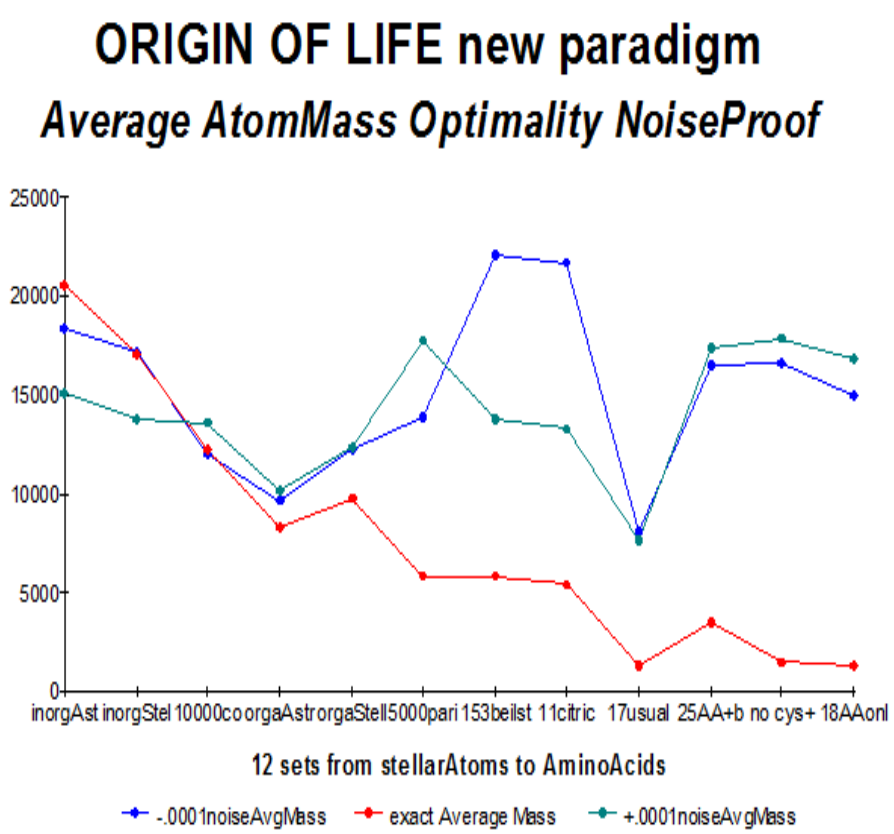
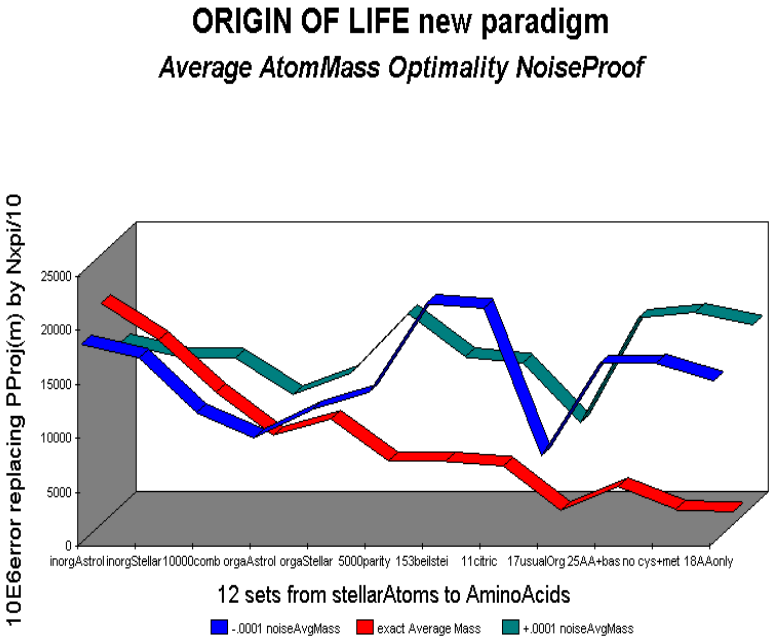
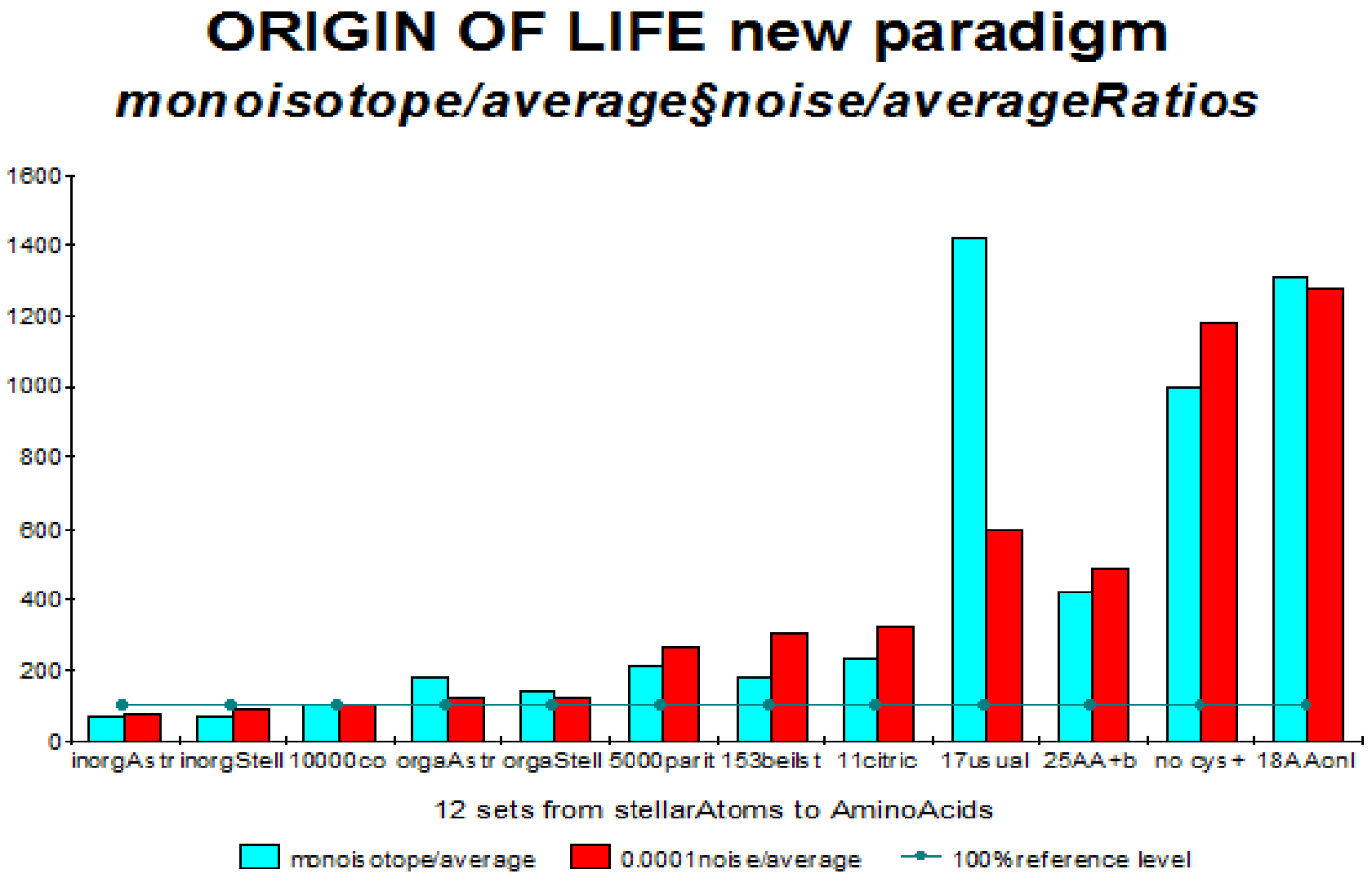




The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:

TIME -IV- TUNING. *The optimized bio-atoms average atomic mass provides the perfect isotopes proportions balancing tuning of Life C O N H bio-atoms then of all DNA, RNA, amino acids components...* ***NOISE or MONO-ISOTOPE effect proof from STELLAR ATOMS... to Earth AMINO ACIDS...***



The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:

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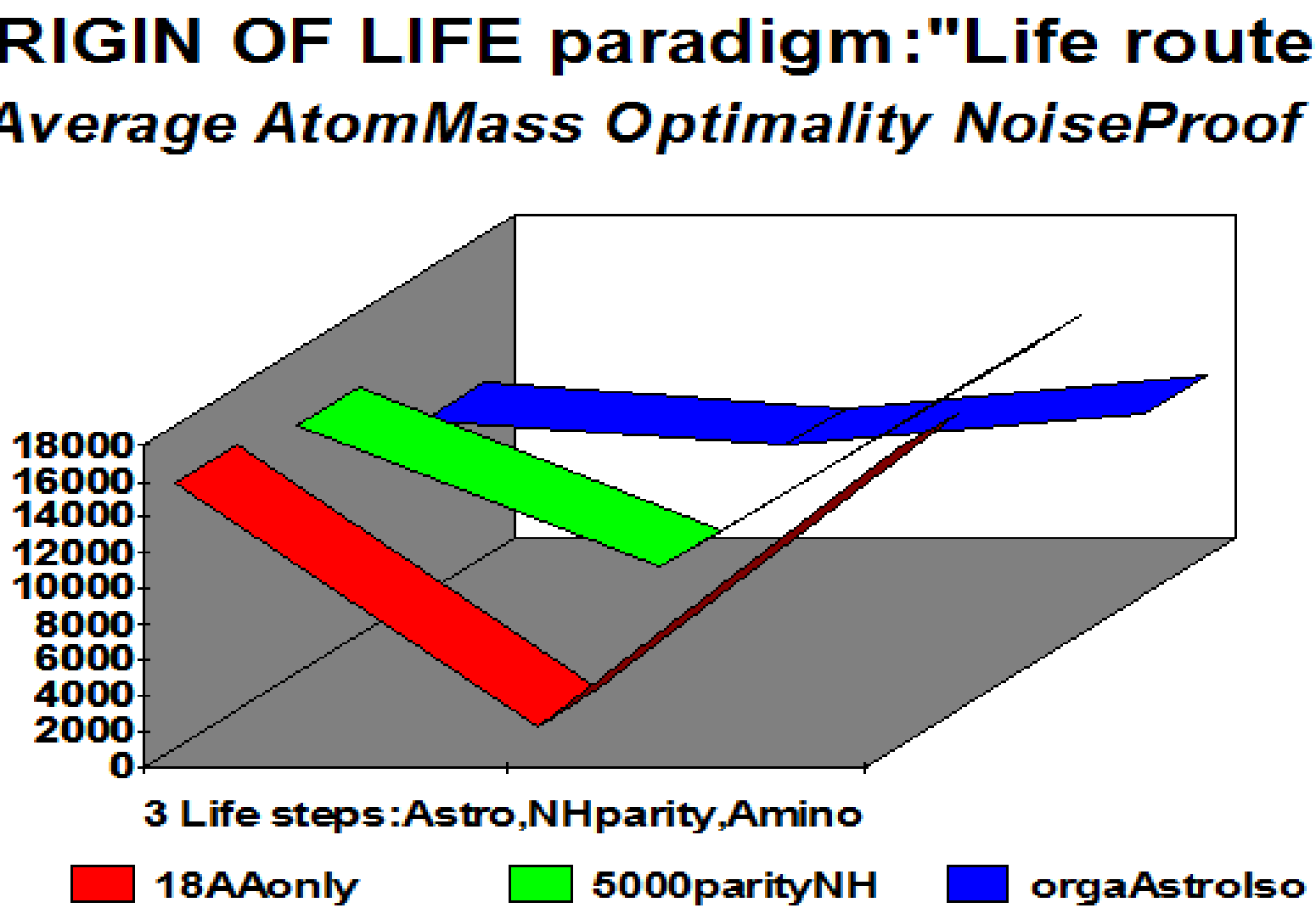
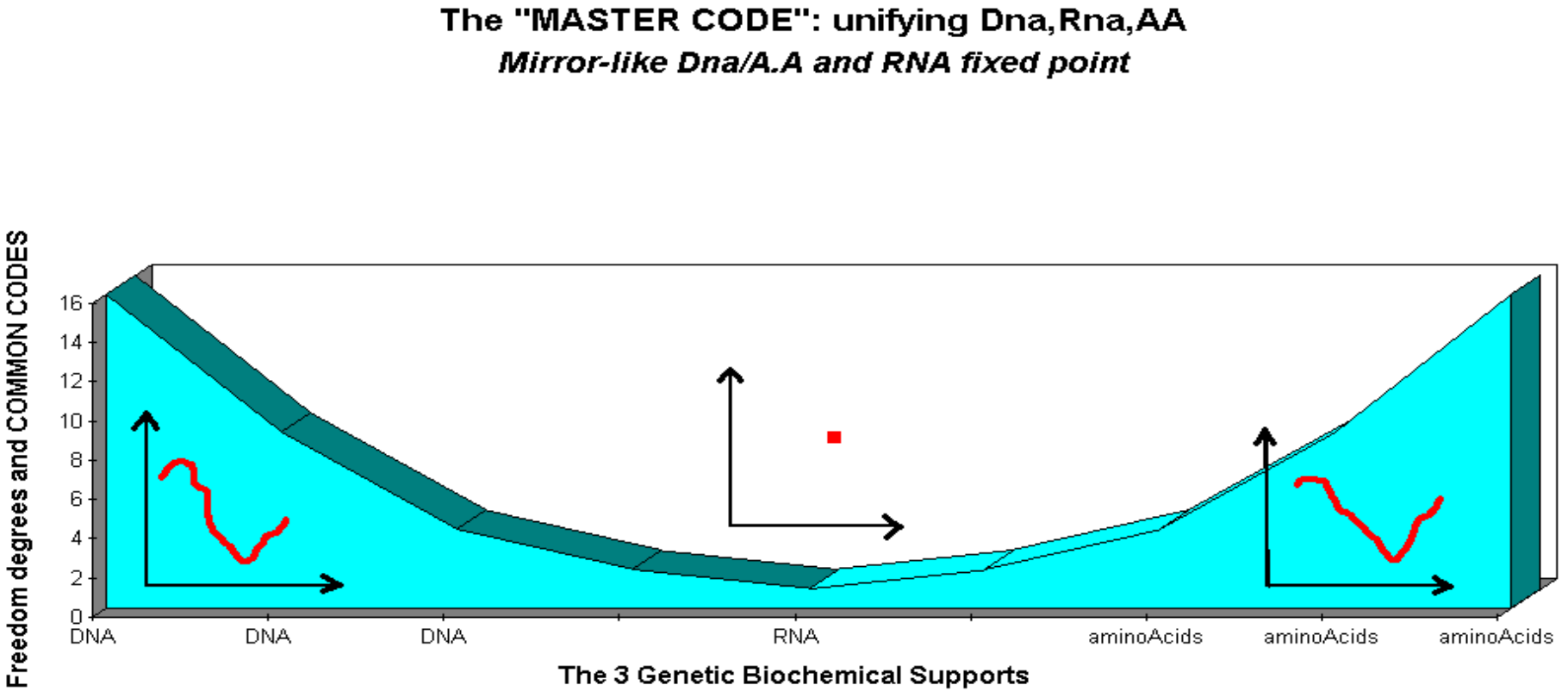
INCREASING OPTIMALITY AND NOISE EFFECT FROM ASTROBIOLOGY ATOMS TO ATMOSPHERIC AMINO ACIDS...



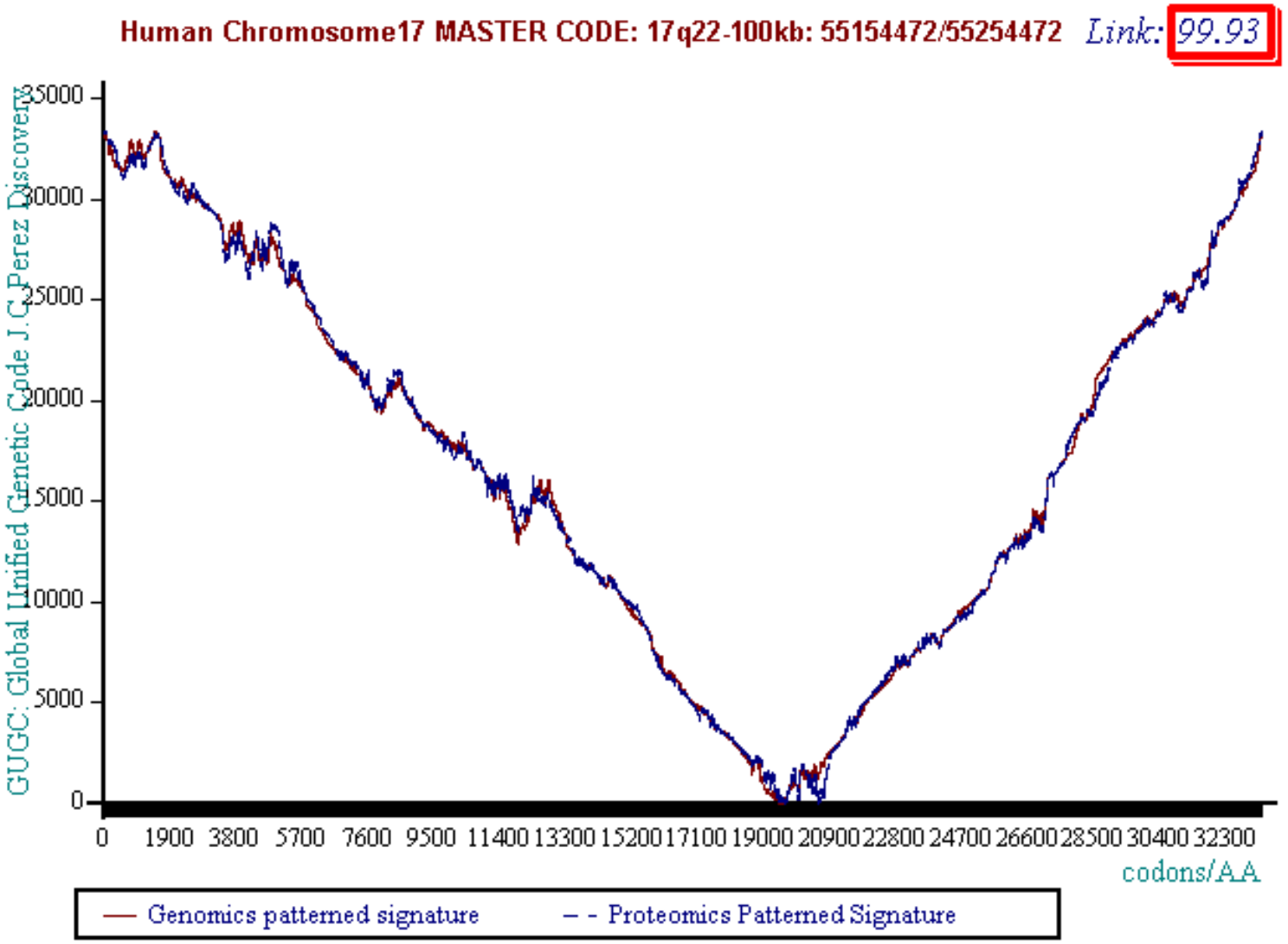
- **The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:**

TIME -V- THE GREAT UNIFICATION. *The DNA, RNA, amino acids GREAT UNIFICATION: CODING (Pi/10 whole numbers) the DNA double strand by codons and its RNA translation and its AMINO ACIDS codons translation (for non coding or coding DNA) provides DNA/AMINO ACIDS correlated patterns and unvariant pattern for RNA!*



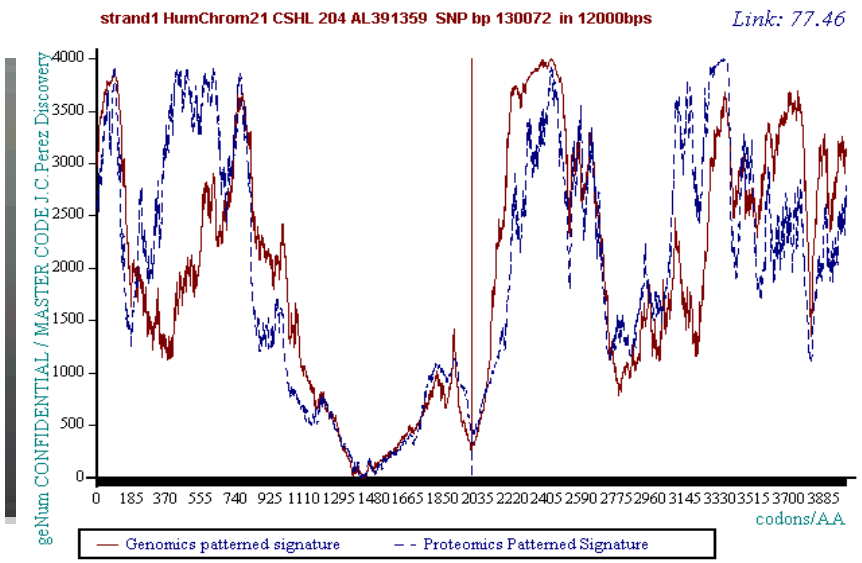
▯ **The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:**

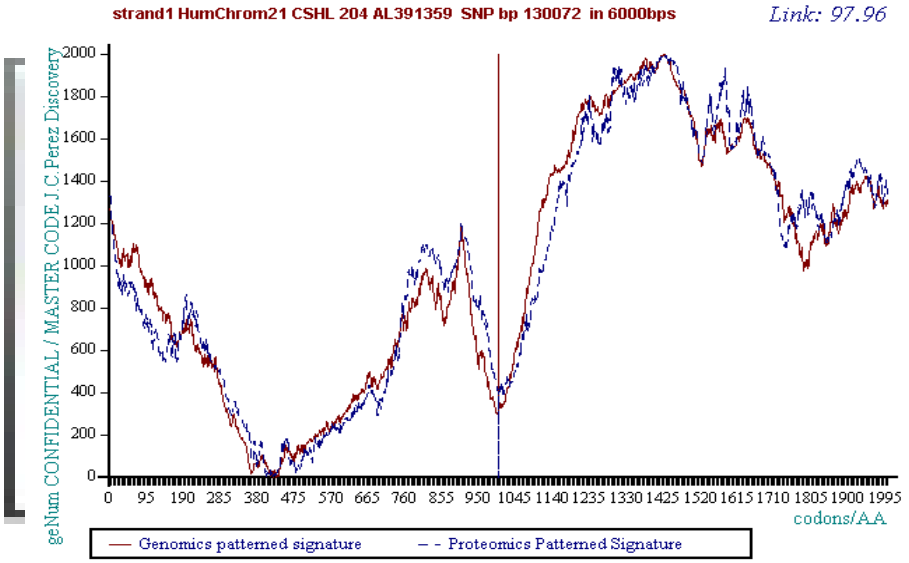
TIME -VI- SYNCHRONIZATION. *The DNA and double stranded patterned images are hightly CORRELATED (for non coding or coding DNA)...*
here an example for a region of HUMAN CHROMOSOME 17...

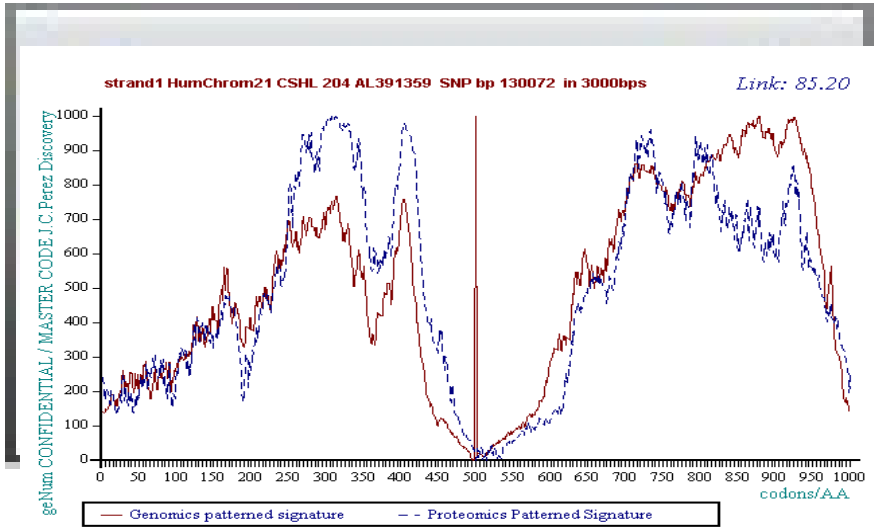


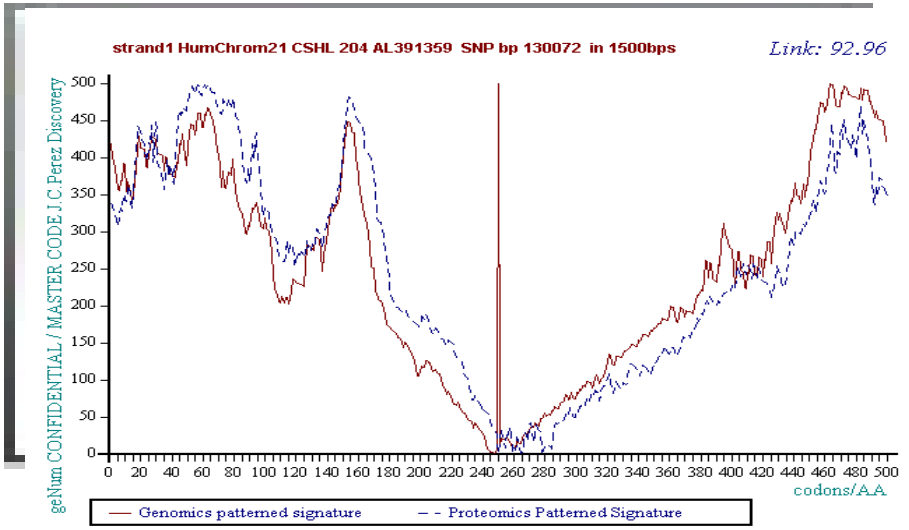
- **The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:**

TIME -VI- SYNCHRONIZATION. *The DNA and double stranded patterned images are hightly CORRELATED (for non coding or coding DNA)...here an example of zooms focusing on a SNP region of 12000bp 6000bp 3000bp 1500bp 750bp*





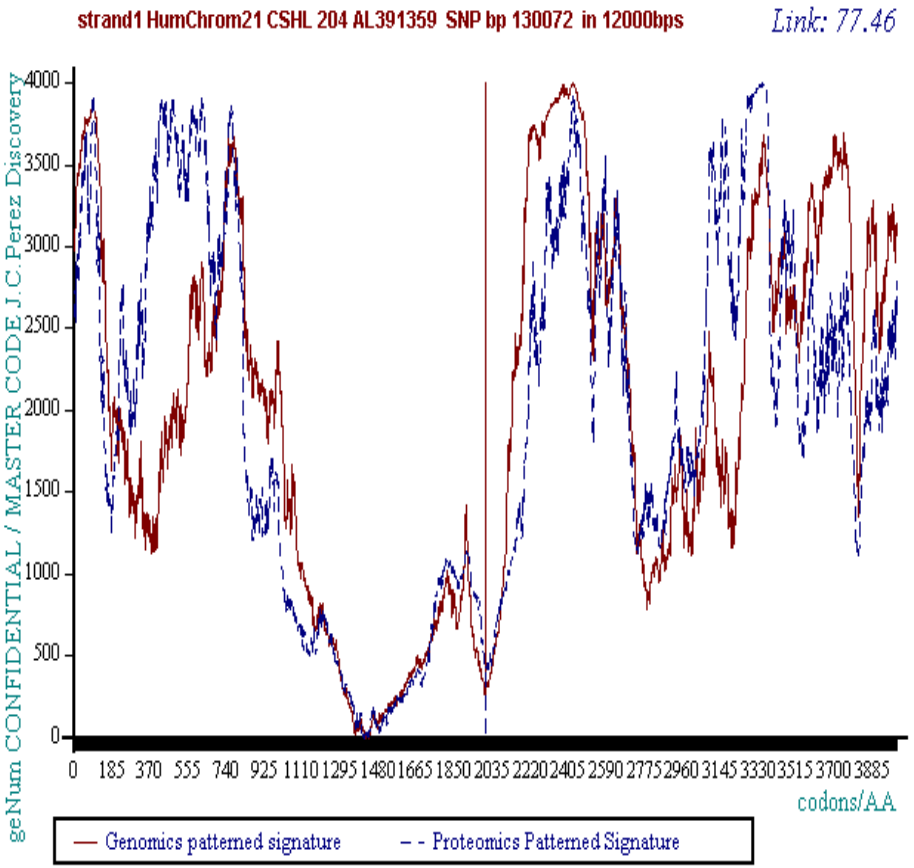


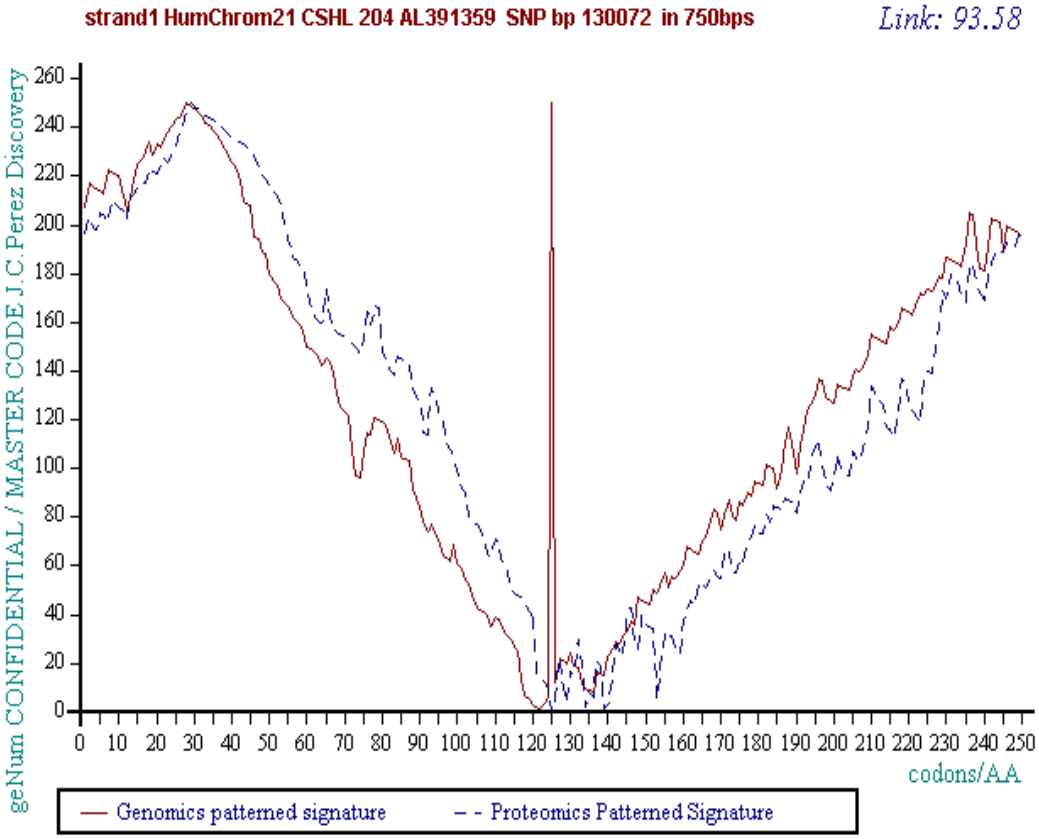


- **The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:**

TIME -VI- SYNCHRONIZATION. *The DNA and double stranded patterned images are hightly CORRELATED (for non coding or coding DNA)...here an example of zooms focusing on a SNP region of 12000bp then zoom on 750bp reveal a rule:*

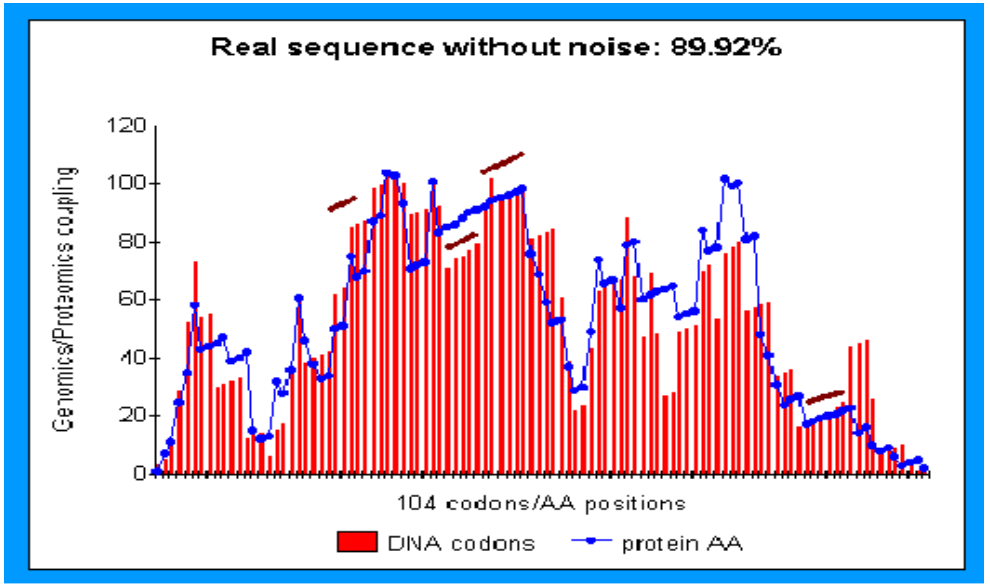
SNP are FUNCTIONAL principally by their LOCATION within GENOMIC DNA!

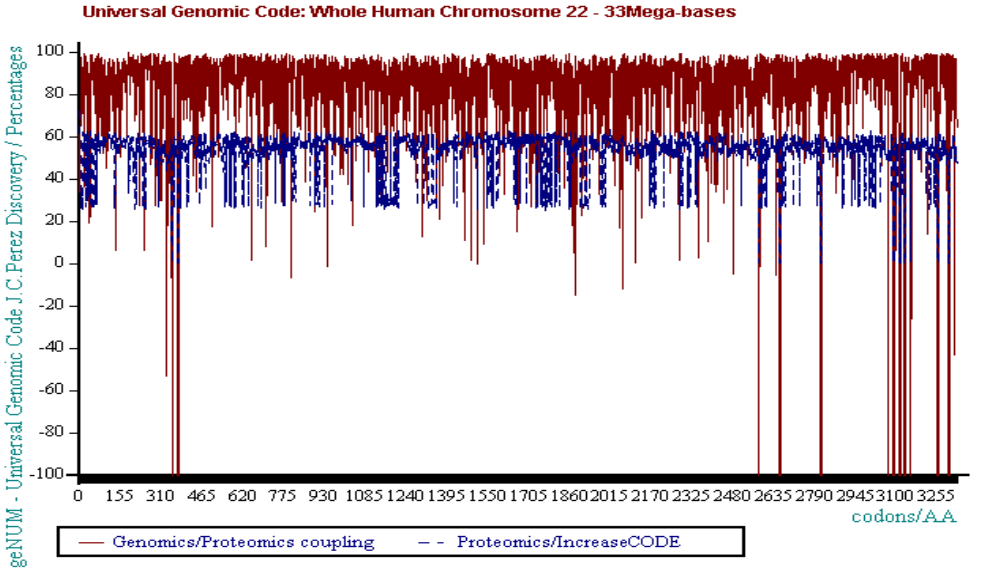


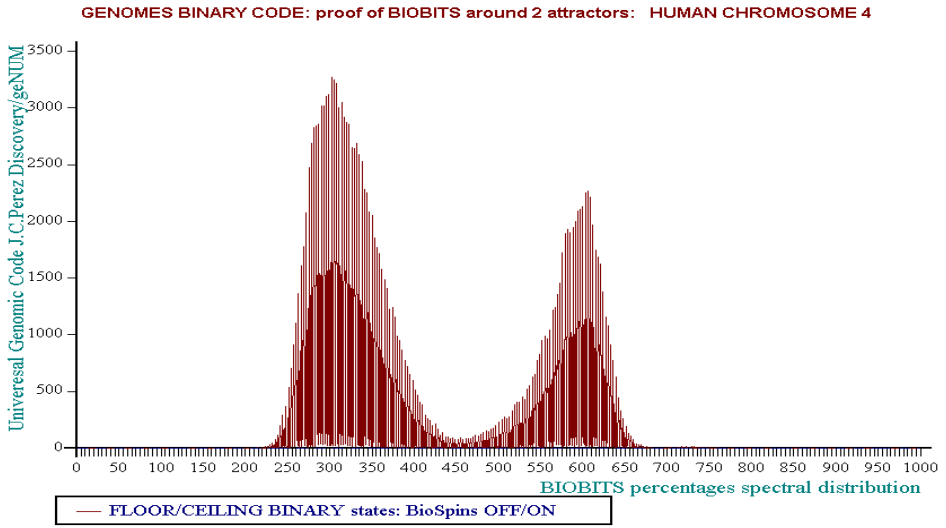


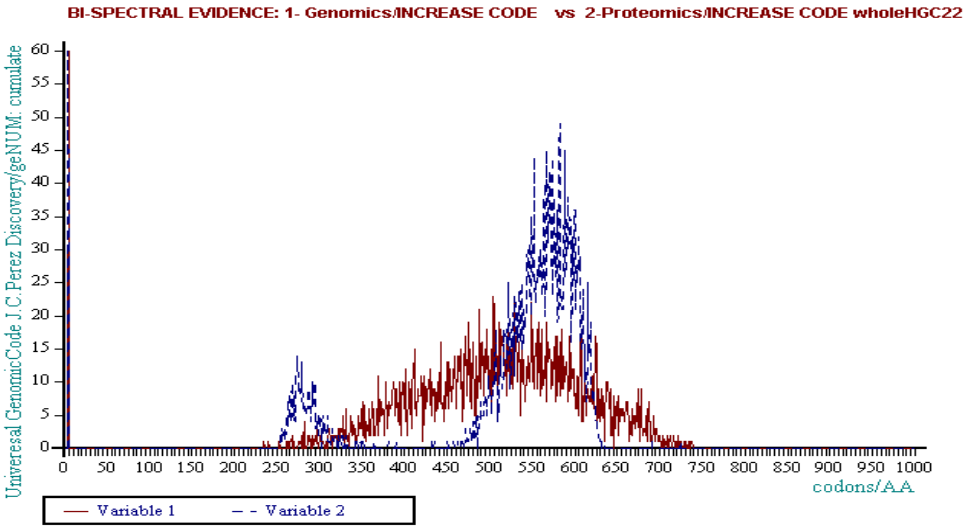
- **The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:**

TIME -VII- DNA BINARY CODE DISCOVERY. *The emergence of a "binary language" from any genomic DNA sequence:* *Analysing on 2D PROTEOMICS images patterns the INCREASE vs DECREASE local dynamics (discrete first order differenciation) then cumulating all increase/decrease values reveals 2 ATTRACTORS.*





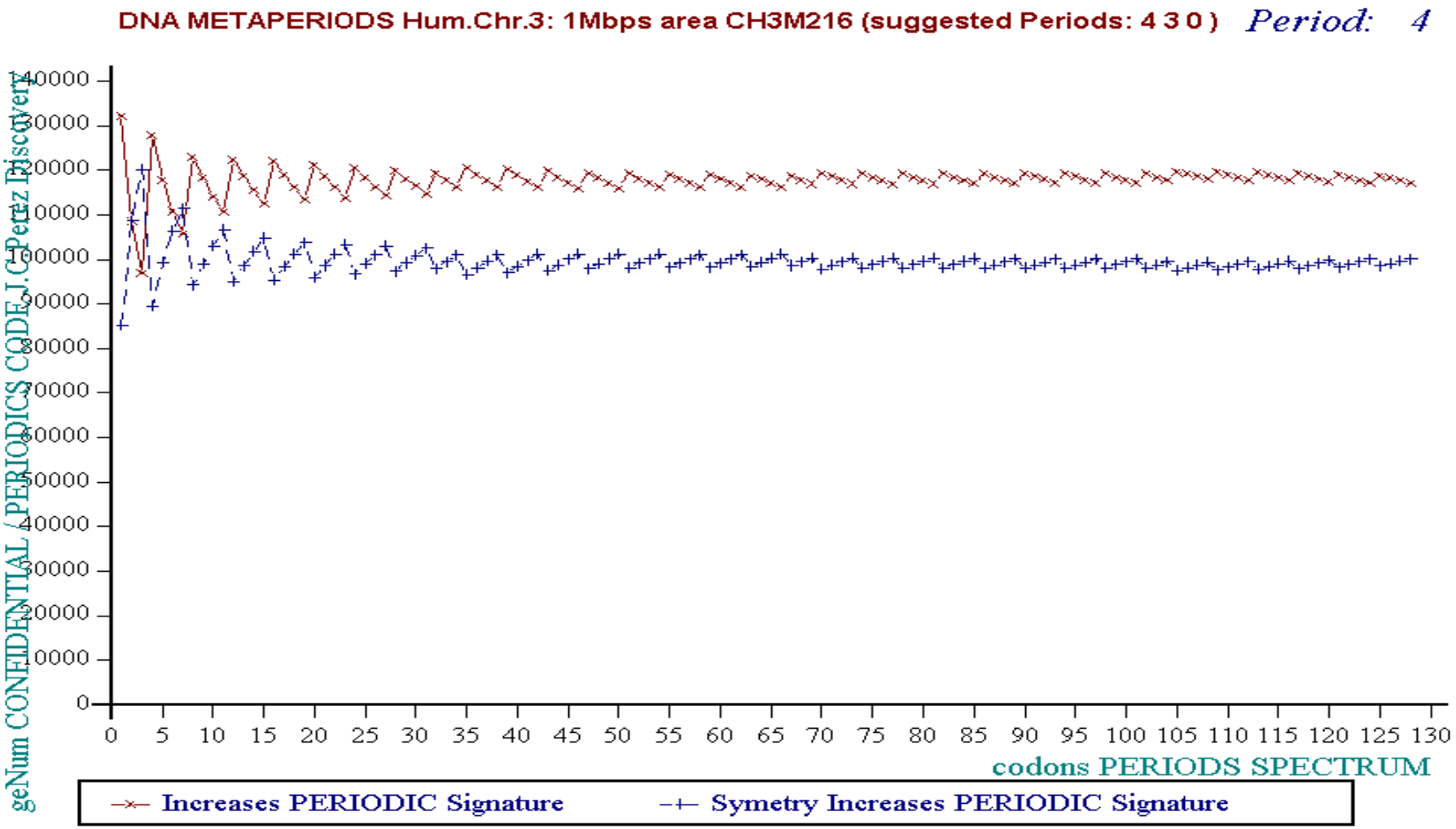




▯ **The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:**

TIME -VIII- DNA DISCRETE SPACIAL WAVES DISCOVERY. ***The emergence of a "WAVESFORMS based language" from any genomic DNA sequence:*** ***Analysing on 2D GENOMICS images patterns the INCREASE vs DECREASE local dynamics of distances 2 3 4... (discrete differenciations of order 2 3 4...) then cumulating all increase/decrease values reveals 2 ATTRACTORS modulated by WAVEFORMS.***

The emergence of undulatory discrete waves overlapping any genomic DNA sequence here example of period=4 in human chromosome



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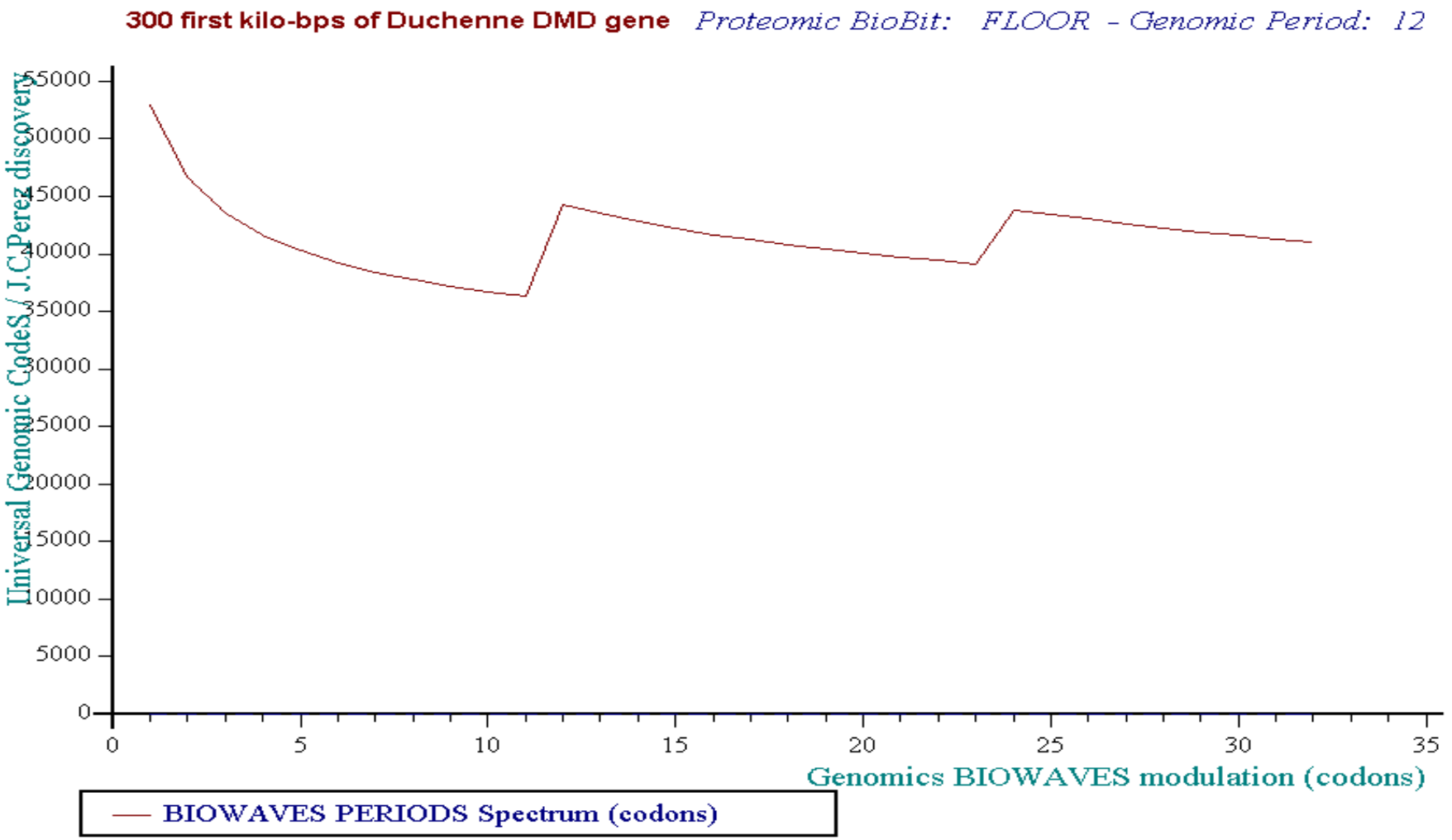
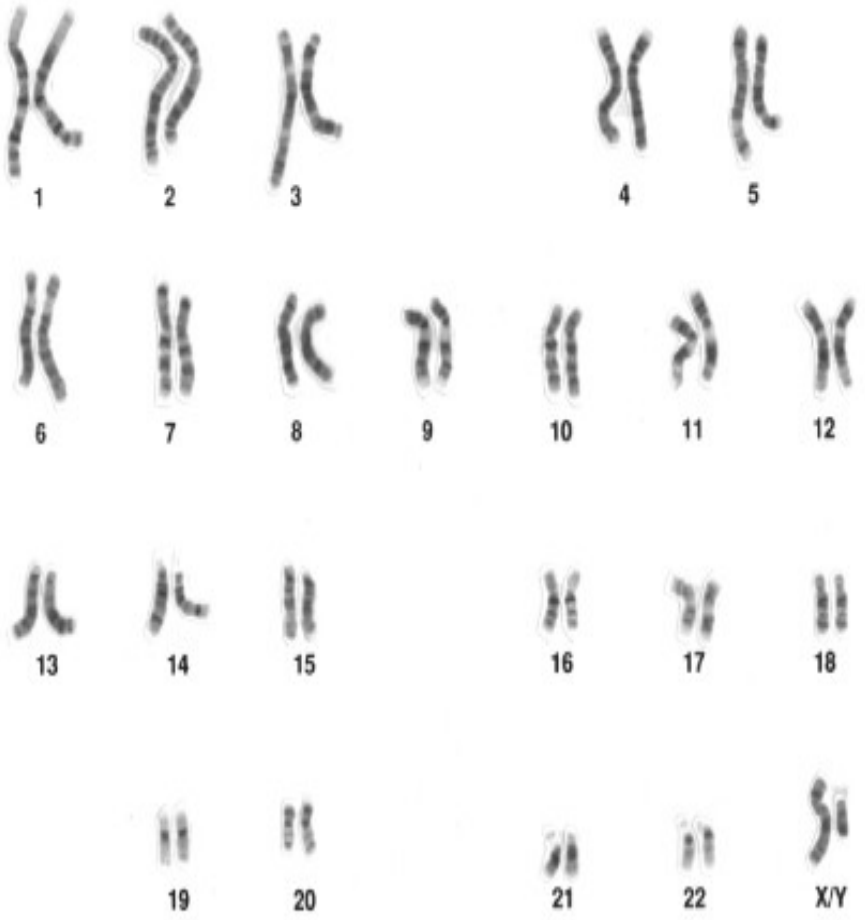
The emergence of undulatory discrete waves overlapping any genomic DNA sequence here example of period=12 in DMD DUCHENNE gene



The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:

TIME -IX- INTERFERENCES BANDING.

The explanation of chromosomal alternated grey bands



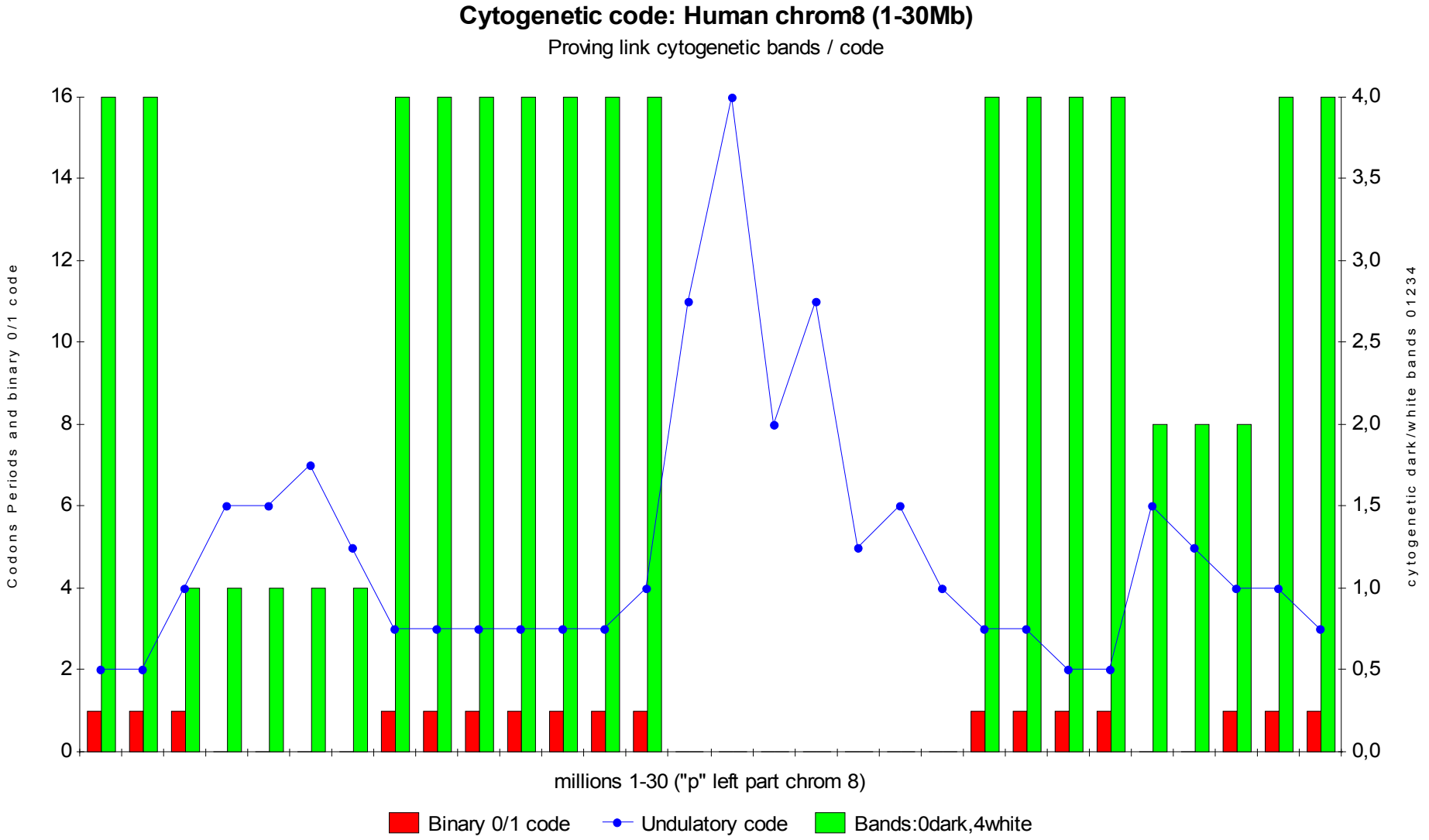
- Analysing such WAVEFORMS on the whole human genome reveals a perfect CORRELATION between the dark/light KARIOTYPES BANDS and the Hight frequencies (periods 2 3) and Low frequencies (periods 4 5 6...)
- From the WAVEFORMS analysis within all human genome double-stranded DNA GENOMICS patterned images.

The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:

TIME -IX- INTERFERENCES BANDING. *The explanation of chromosomal alternated grey bands: example in human chromosome 8 region: combining binary code and waveforms reveals kariotypes bands:*

binary code=1 and hight frequencies ==> WHITE bands

binary code=0 and low frequencies ==> DARK bands

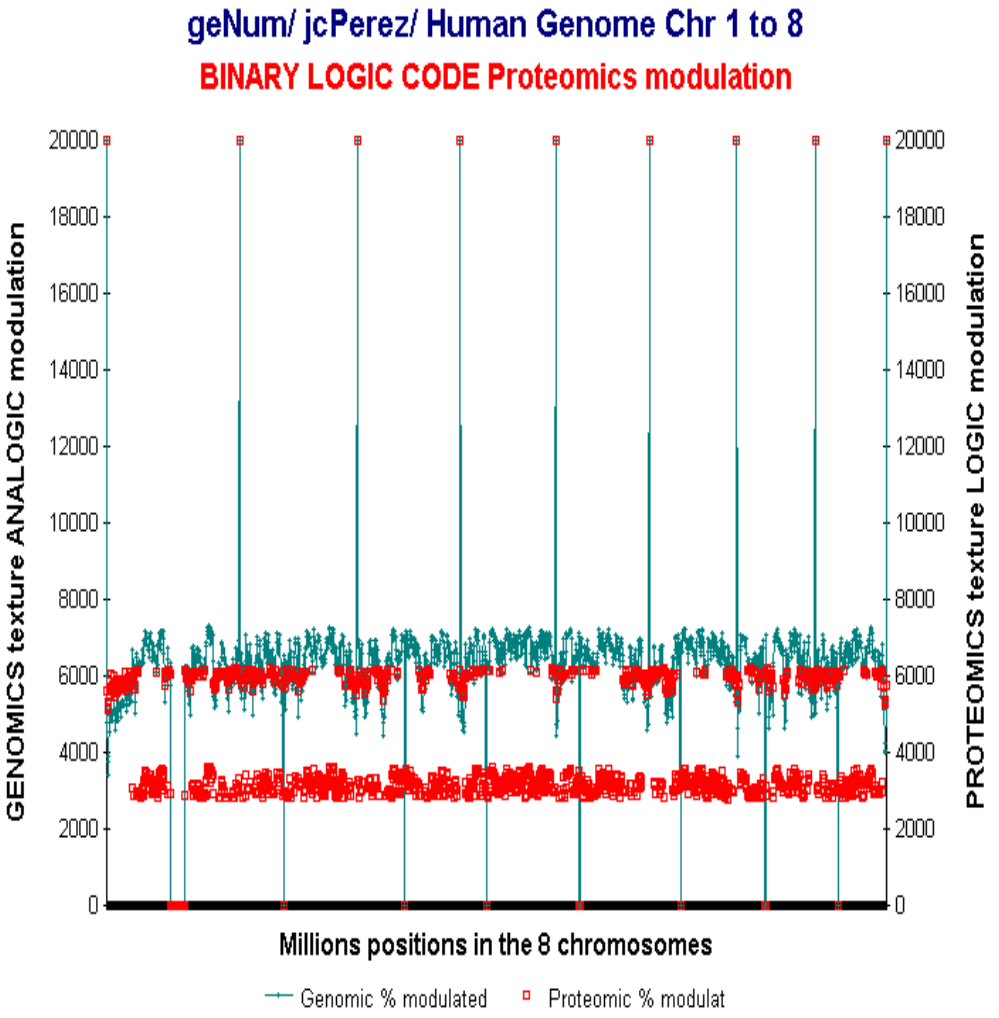


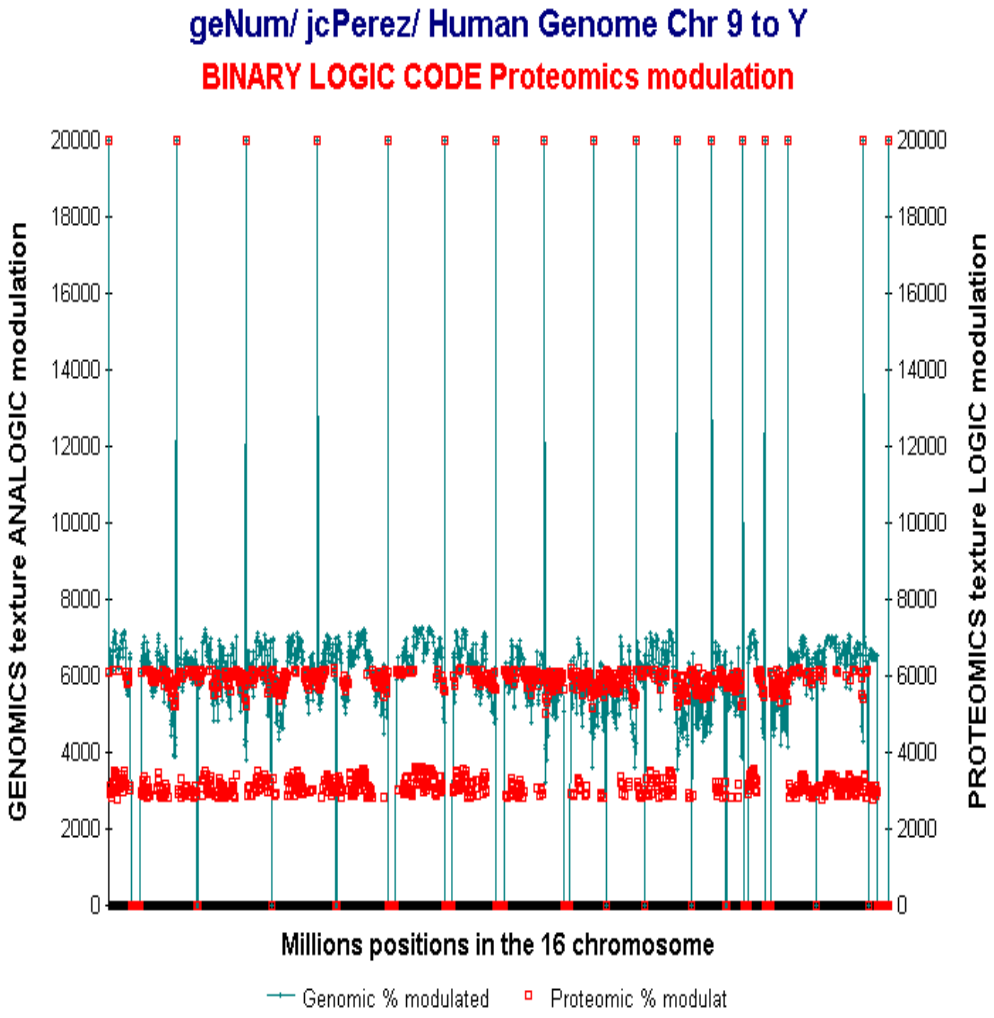
The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes:

TIME X – GOLDEN RATIO CONTROLS THE WHOLE HUMAN GENOME...

The 2 "golden ratio" attractors of the whole human genome

The EVIDENCE of BINARY PROTEOMICS CODE(red) and MODULATED GENOMICS CODE (blue) at WHOLE HUMAN GENOME SCALE!





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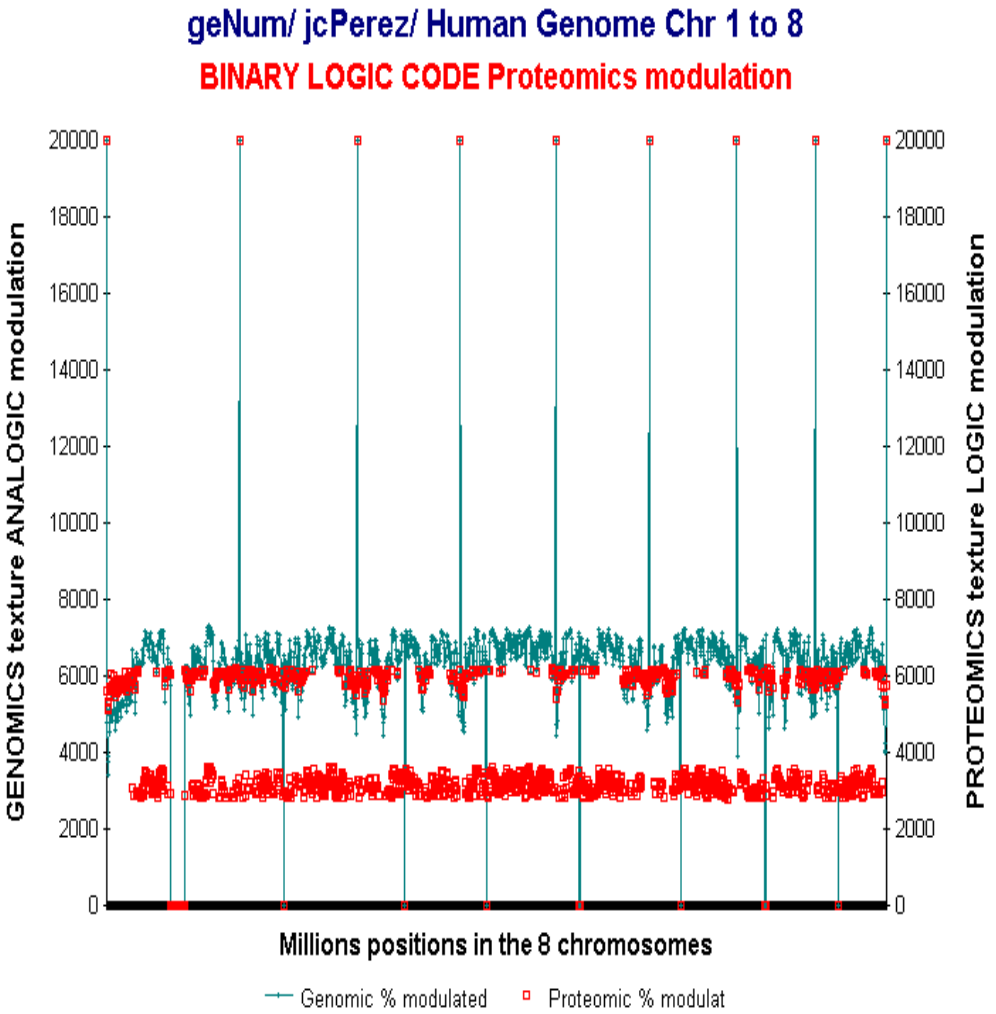


The Whole Human Genome Binary Code:

"The whole Human Genome is controled by two BINARY CODES ATTRACTORS which provide a kind of self-organized bistable binary code ... like in computers! With the central following difference:

-the binary code within computers was invented artificially by humans...

-the binary code of DNA has "emerged" spontaneously ...

MEANWHILE, there is a fact:

-The ratio between both bistable states is exactly equal to "2" (the space between two consecutives octaves in Music...)

-The Top state is exactly matching with GOLDEN RATIO...

-The Bottom state is also exactly related to Golden Ratio...

« Top » level = phi = 1 / PHI

« Bottom » level = phi / 2 = 1 / 2 PHI

Top / Bottom = 2

Where PHI is the « Golden Ratio"...

The great Unification: Unifying DNA, RNA and Amino acid worlds from bioatoms to whole Genomes: Part III - FUTURES:

Perspectives in Luc Montagnier's *« DNA Waves and Water »* breakthrough Luc Montagnier ,Lindau

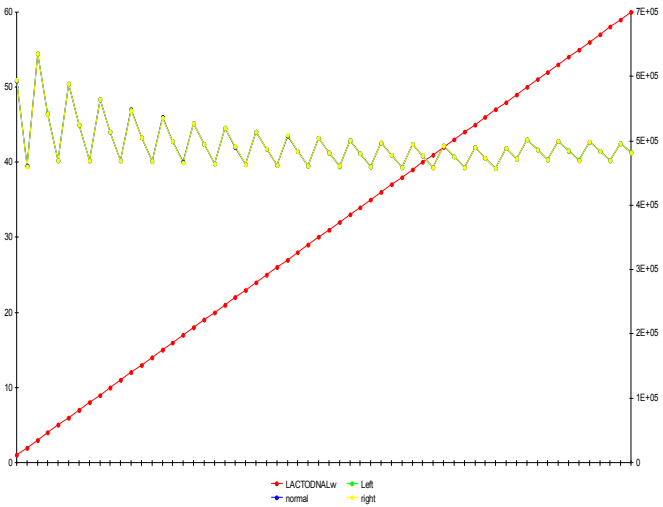
NOBELS conference, 28 June, 2010 - DNA BETWEEN PHYSICS AND BIOLOGY: « DNA WAVES AND WATER »

2 strong relations between our research and DNA waves and water results:

« 7.83 Hertz Schumann Earth background Resonance and DNA spatial waveforms strong relationships »

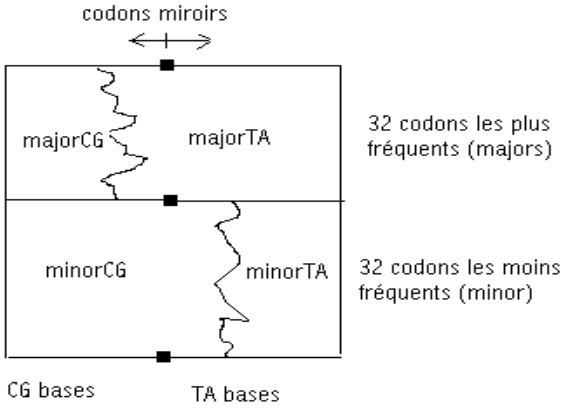
In his Nobel Lindau conference, Pr Montagnier reports emergence of electromagnetic waves for specifics DNA like HIV genes but, in others cases, like LACTOBACILLUS bacteria, these waveforms are not observed. Secondly, these waves are only observed when they are « boosted » by the earth atmospheric ground waveform: SCHUMANN RESOMANCE = 7.83 Hertz. Then we correlated both facts with our research:

1/ we associated **Montagnier's waves ON with our LOW FREQUENCIES** (exp HIV or BORRELIA top right high frequencies image shows a 8 codons low frequency period) and **Montagnier's waves OFF with our HIGH FREQUENCIES** (exp LACTOBACILLUS bottom right high frequencies image shows a 3 codons high frequency period). As described in the CODEX BIOGENESIS book (jc perez 2009), HIGH FREQUENCIES are 2 or 3 codons periods waves and 4 5 6...12... are LOW FREQUENCIES.



2/ 7.83 Hertz Schumann Earth background Resonance and DNA strong relationships: In the whole HUMAN GENOME single stranded DNA, if we consider 2 clusters of 32 codon populations each, the most frequent (Q1+Q2) is exactly 2X as numerous as the least frequent of the 32 codons (Q3+Q4) . Exact ratio is 1.995859355...This fact is ALSO verified at atomic weights level. Then, what about TA versus CG quartiles composition? Now we call these 4 quartiles: MajorTA minorTA MajorCG and minorCG.

(Major TA x minor CG) / (minor TA x Major CG) = 3.8184783551 = Schumann resonance / (Phi x racine Phi) and also: (Major CG x minor TA) / (minor CG x Major TA) = Schumann resonance / 30 = 0.261. In both cases, relative errors are around 1/10000.



(majorCG / minorCG) / (majorTA / minorTA) = Phi2/10

BIT Life Sciences' 3rd World Congress of Vaccine
Beijing·China

Session Name: Section 2-2-1: Bioinformatics, Antigen Design, and Vaccine Development

Decoding non-coding Dna Codes: Human Genome Meta-Chromosomes Architecture

*Dr. Jean-Claude Perez** Individual Researcher, Bordeaux, France

ACKNOLEDGEMENTS to Pr ***Luc Montagnier*** *FMPRS*
World AIDS Foundation UNESCO
and ***Jean-rené Fourtou*** *Vivendi Universal chairman*

More on: http://golden-ratio-in-dna.blogspot.com/